Database :	Searched:	Scoring table:	Title: Perfect score: Sequence:	Run on:	OM protein - pr	
SPTREMBL_10:* 1: sp_archea:* 2: sp_bacteria:* 4: sp_fungi:* 5: sp_fundan:* 5: sp_invertebrate:* 6: sp_mammal:* 7: sp_mbc:* 8: sp_organelle:* 9: sp_phage:* 10: sp_plant:* 11: sp_rodent:* 12: sp_virus:* 13: sp_virus:* 14: sp_unclassified:*	201082 seqs, 61543640 residues	BLOSUM62	US-09-104-063-4 1830 1 MEGISIYTSDNYTEEMGSGDKRGGHSSVSTESESSSFHSS 352	September 14, 1999, 09:51:02; Search time 16.15 Seconds (without alignments) 1341.385 Million cell updates/sec	- protein search, using sw model	GenCore version 4.5 Copyright (c) 1993 - 1998 Compugen Ltd.

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

25 27 28 29	19 20 21 22 23 24	11111111111111111111111111111111111111	Result
500 500 500 500 500	0000	1816 1548.5 1386.5 11161 1121.5 574.5 574.5 574.5 574.5 574.5 574.5 574.5 574.5 574.5 574.5 574.5 574.5 574.5	Score
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ALIGNMENTS

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233 QKRKALKTTVILILAFFACWLPYYIGISIDSFILLEIIKQGCEFENTVHKWISITEALAF 292 	173 IFANVSEADDRYICDRFYPNDLWVVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGH 232 	113 HVIYTVNLYSSVLILAFISLDRYLAIVHATNSQRPRKLLAEKVVYVGVWIPALLLTIPDF 172 	53 IVGNGLVILVMGYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAV 112 	1 MEGISIYTSDNYTEEMGSGDYDSMKEPCFREENANFNKIFLPTIYSIIFLTG 52 	Query Match 99.2%; Score 1816; DB 4; Length 360; Best Local Similarity 97.8%; Pred. No. 2.3e-138; Matches 352; Conservative 0; Mismatches 0; Indels 8; Gaps	coupled receptor; Transmembra 360 AA; 40607 MW; 110EB9E6	FAM; PF00001; 7tm ROSITE; PS00237;	IMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED AJ224869; CAA12166.1;	tt. 426:271-278(1998)	mic organization and promoter characterization	CARUZ A., SAMSOM M., ALONSO J.M., ALCAMI J., BALEUX F., VIRELIZIER J.L., PARMENTIER M., ARENZANA-SEISDEDOS F.;	NCE FROM N.A. NE; 98258970.	Eucheria, Frimaces, Cacallilli) nominidae; nomo:	ч	CXCR4.	GENE ENCODING RECEPTOR CXCI	07, Las	60835; 1-AUG-1998 (TrEMBLrel.	060835 PRELIMINARY; PRT; 360 AA.	35 1

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01-NOV-1998
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Q62973;
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Eukaryota; Metazoa; Chordata; Cr
Eutheria; Primates; Catarrhini;
                                                            01-NOV-1996 (TrEMBLrel.
01-NOV-1996 (TrEMBLrel.
01-MAY-1999 (TrEMBLrel.
CHEMOKINE RECEPTOR LCR1.
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MURAYAMA Y., MATSUNAGA S., INOUE-MURAYAMA M.;
"CDNA sequence of African green monkey CXCR-4
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Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Eutheria; Rodentia; Sciurognat
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i; Cercopithecidae; Cercopithecinae;
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Best Local
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-!- SIMILARITY: bull

-!- SIMILARITY: bull

EMBL; Y17895; CAA76924.1; -.

EMBL; Y17894; CAA76923.1; -.

PROSITE; PS00237; G_PROTELN_RECEPTOR; 1.

PROSITE; PS00237; G_PROTEDLA receptor; Transmembrane;

PSCPEDTOR; G-PROTECIN COUPLED RW; E991FD1D CRC32;
                                                                                                                                                                                                                                                                                                                                                     Q9YGC3;
Q9YGC3;
01-MAY-1999
                                                                                                           MOEPPS B., KNOEPFLE K., BROWN M., KNOECHEL W., GIERSCHIK P.;
"Expression of the CXC chemokine receptor 4 during early Xenc
laevis embryogenesis: a possible role of chemokine receptors
regulators of development and differentiation.";
Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMII
-!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECE
                                                                                                                                                                                                                                                                                                                       01-MAY-1999 (TrEMBLrel.
01-MAY-1999 (TrEMBLrel.
01-MAY-1999 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- SUBČELLULAR LÓCÀTION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
EMBL; U54791; AABO1981.1; -.
PFAM: PF00001; 7tm_1; 2.
PROSITE; PS00237; G_PROTEIN_RECEPTOR; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein.
SEQUENCE 332 AA; 37442 MW; COEAB84B CRC32;
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SEQUENCE FROM N.A.
STRAIN-SPRAGUE-DAWLEY;
                                                                                                                                                                                                                                              Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Vertebrata; Amphibia; Bat
Mesobatrachia; Pipoidea; Pipidae; Xenopodinae; Xenopus.
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                                                                                                                                                                                                                                                                                               CXCR4
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Psych. 0:0-0(0)
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6; Mismatches 16;
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Query Match Best Local Similarity

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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRÂNE PROTEIN (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
EMBL; AJ001039; CAA04493.1; -
PFAM; PF00001; 7tm_1; 1.
PROSITE; PS00237; G_PROTEIN_RECEPTOR; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein.
SEQUENCE 357 AA; 39817 MW; 6D892EFE CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;
Neopterygii; Teleostei; Euteleostei; Protacanthopterygii;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DANIELS G.D., CHARLEMAGNE J., SECOMBES "Cloning and sequencing of a rainbow to chemokine receptor homolog.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
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                                                                                                 LILAFISMDRYLAVVHATKSQSTRTFLADRVIYVAVWLPAVILTVPDIVFATALDGGSRT
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01-MAY-1999
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093247;
01-NOV-1998
01-NOV-1998
01-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                                                            *FUJIKI K., NAKAO M., SHIN D., YANO T.;

*CDNA cloning of a carp homologue of mammalian CXCR4.";

*Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.

-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).

-!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.

EMBL; ABOL3310; BAA32797.1; --

PRAM; PF00001; 7tm_1; 1.

PROSITE; PS00237; G_PROTEIN_RECEPTOR; 1.

G-protein coupled receptor; Transmembrane; Glycoprotein.

SEQUENCE 353 AA; 39633 MM; 23DD5347 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cyprinus carpio (Common carp).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Neopterygii; Teleostei; Euteleostei; Ostariophysi;
Cyprinoidea; Cyprinidae; Cyprininae; Cyprinus.
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3 (TrEMBLrel. 0
9 (TrEMBLrel. 1
RECEPTOR CXCR3.
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Last sequence update)
Last annotation updat
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Last sequence update)
Last annotation updat
                                                       PRT;
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CHEMOKINE

RECEPTOR

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RESULT
O15185
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AC 01
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DT 01
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RP G
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Best Local Similarity 35.0%;
Matches 121; Conservative 7
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Best Local Similarity
Matches 120; Conserv
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SOTO H., WANG W., STRIETER R.M., COPELAND N.G., J., JENKINS N.A., HEDRICK J., ZLOTNIK A.;

"The CC chemokine 6Ckine binds the CXC chemokine receptor CXCR3.";

Proc. Natl. Acad. Sci. U.S.A. 95:8205-8210(1998).

EMBL; AF045146; AAC40163.1;

PFAM; PF00001; 7fm_1; 1.

PFAM; PF00001; 7fm_1 4.

267 AA: 41016 MW; 037CB161 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        O15185 PRELIMINARY; PRT; 415 AA.
O15185;
O1-JAN-1998 (TrEMBLrel. 05, Created)
O1-JAN-1998 (TrEMBLrel. 05, Last sequence update)
O1-NOV-1998 (TrEMBLrel. 08, Last annotation update)
G PROTEIN-COUPLED RECEPTOR CKR-L2.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Entheria: Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                              GUTIERREZ J., VARONA R., ZAB/
Submitted (SEP-1996) to the I
EMBL; 279783; CAB02143.1; -.
PFAM; PF00001; 7tm_1; 1
                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        325
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                                                                                                                DNYTEEMGSGDYDS----MKEPCFREENANFNKIFLPTIYSIIFLTGIVGNGLVILVMGY 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VCWTPYHLYVLYDILMDVGVLARNCGRKSHVDVAKSVTSGMGYMHCCLNPLLYAFVGVKF
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QKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNLYSSVL
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                                                         ENFSSSYDYGENESDSCCTSPPCPQDFSLNFDRAFLPALYSLLFLLGLLGNGAVRAVLLS 127
                                                                                                                                                                                                                                                                                                                            415 AA;
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                                                                                                                                                                                                                                                                                                                         45608 MW;
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The EMBL/GenBank/DDBJ
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Pred. No. 4.8e-39;
'1; Mismatches 133
                                                                                                                                                                          Score 574.5; DB
Pred. No. 1e-38;
); Mismatches 1
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Best Local
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MEDLINE; 99077268.

MEDLINE; 99077268.

MARONA R., ZABALLOS A., GUTIERREZ J., MARTIN P., ROLVARONA R., ZABALLOS A., GUTIERREZ J., MARTIN P., ROLVARONA R., ZABALLOS A., GUTIERREZ J., MARTIN P., ROLVARONA R., MARQUEZ G.;

Molecular cloning, functional characterization and analysis of the murine chemokine receptor CCR6 and ligand MIP-3alpha.";

PEBS Lett. 440:188-194(1998).

EMBL; AB009369; BAA23776.1; -.

EMBL; AB009369; BAA23776.1; -.
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                                                                                                                                                                                                                                                                                                                                                                        2
                                                                                                                                                                                        YSSVLILAFISLDRYLAIVHATNS--QRPRKLLAEKVVYYGVWIPALLLTIPDFIFANVS 178
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                                                    ELQDRDVCEPRYRSVSEPITWKLLGMGLELFFGFFTPLLFMVFCYLFIIKTLVQAQNSKR
                                                                                                   EADDRYICDRFYPN----DLWVVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQK
                                                                                                                                                             NCGMLLLACISMDRYIAIVQATKSFRVRSRTLTHSKVICVAVWFISIIISSPTFIFNKKY
                                                                                                                                                                                                                                                                  TFAFYKKARSMTDVYLLNMAITDILFVLTLPFWAVTHATNTWVFSDALCKLMKGTYAVNF
                                                                                                                                                                                                                                                                                           VMGYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAVAN-WYFGNFLCKAVHVIYTVNL 120
                                                                                                                                                                                                                                                                                                                                                                           NSTESYFGTDDYDNTEYYSIPPDHGPCSLEEVRNFTKVFVPIAYSLICVFGLLGNIMVVM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (DEC-1997)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   367 AA; 42102 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (Mouse).
|etazoa; Chordata; Craniata; Ver
|dentla; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KOMURA E., -1997) to the
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ne EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 63;
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3 2. T
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ae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 11;
.5e-38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 128;
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Best Local :
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  093281;
093281;
01-NOV-1998
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                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN-BREED BEAGLE;
                                                                                                                                                                                                                                                                                                                                                                                                                              Canis familiaris (Dog).
Eukaryota; Metazoa; Chordata;
                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                    Submitted (FEB-1998) to the EMBL; AF047047; AAC98968.1;
                                                                                                                                                                                                                                                                                                                                                                                      CHANG Y.F., NOVOSEL V.,
                                                                                                                                                                                                                                                                                                                                                                                                                      Eutheria; Carnivora; Fissipedia;
                                                                                                                                                                                                                                                                                                                                                                               The
                                                                                                                                                                                                                                                                                                                                                                                                                                               INTERLEUKIN-8 RECEPTOR.
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                                                           STTF
                                                                           SSSF
                                                                                                    AFFHCCLNPILYAFLGAKF-----KTSAQHALTSVSRGSSLKILSKGKRGGHSSVSTESE
                                                                                                                                  GHQKRKALKTTVILILAFFACWLPYYIGISIDSFILLEIIKQGCEFENTVHKWISITEAL
                                                                                         GFFHSCLNPLIYAFIGQKFRHGLLKIMAFHGLI-----SKEYLPKDSRPSFVGSSSANT
                                                                                                                          MGQKHRAMRVIFAVVLVFLLCWLPY--NLVADTLMRLQAIEETCQRRNDIGRALDATEIL
                                                                                                                                                                                          VNFYSGILLLASISMDRYLAIVHATRRLTQKKHWV-KFICLGIWALSLILSLPIFVFRRA
                                                                                                                                                                                                          VNLYSSVLILAFISLDRYLAIVHATNSQRPRKLLAEKVVYVGVWIPALLLTIPDFIFAN-
                                                                                                                                                                                                                           LVILVMGYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYT 117
                                                                                                                                                                                                                                                                             DNYTEEMGSGDYDSM-----
                                                                                                                                                                                                                                                                                                                                                                             isolation and sequence of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HRAIRVVIAVVLVFLACQIPH-----NWVLLVTAVNTGKVGRSCSTEKVLAYTRNVAEV
                                                                                                                                                            INPPYSSPVC-
                                                                                                                                                                          VSEADDRYICDREYPNDLWVVVFQFQHIM-----VGLILPGIVILSCYCIIISKLSHSK
                                                                                                                                                                                                                                                           DNYSLEDLFGDIDNYTYNTEMPIIPADSAPC-RPESLDINKYAVVVIYVLVFVLNLLGNS
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                                                                                                                                                                                                                                                                                             128;
                                                                                                                                                                                                                                                                                                     Similarity
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                                                                                                                                                                                                                                                                                                                                     356 AA;
  (TrEMBLrel.
                   PRELIMINARY;
                                                                                                                                                                                                                                                                                             Conservative
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                                                                                                                                                          ----YEDMGTNTTKLRIVMRALPQTFGFIVPLMIMLFCYGLTLRTLFEAH
                                                                                                                                                                                                                                                                                                                                     40505
                                                                                                                                                                                                                                                                                                     30.8%;
35.2%;
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                                                                                                                                                                                                                                                                                           Score 564; DB Pred. No. 6.2e-59; Mismatches
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                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                     Craniata; Vertebrata; Mammalia;
ia; Canidae; Canis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                     C.F.;
                                                                                                                                                                                                                                                                                                                                                                              canine
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                   392
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Similarity

29.3%; 30.7%;

Score Pred.

535.5; DB 1 No. 1.3e-35;

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Query Match
Best Local Similarity
Matches 118; Conserv
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"Molecular cloning of a novel c
stage chick embryos",
Biochem. Mol. Biol. Int. 44:673
EMBL; AF029369; AAC23950.1; -
PFAM; PF000001; 7tm.1; 2
SEQUENCE 392 AA; 44760 MW;
                                                                                                                                                                                                                                                                                                            008707;
                                                                                                                                         Mus musculus (Mouse).
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eurtheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                01-JUL-1997 (TrEMBLrel. 04, Created)
01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation updat
CHEMOKINE (C-C) RECEPTOR 9 (BETA-CHEMOKINE RECEPT
               NIBBS R.J.B., WYLIE S.M., PR. Submitted (MAY-1997) to the EMBL; Y12879; CAA73379.1; -. MGD; MGI:1096320; CMKBR9. PFAM; PF00001; 7tm_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1998 (TREMBLrel. 08, 01-MAY-1999 (TREMBLRel. 10, PUTATIVE CHEMOKINE RECEPTOR. CRL1.
 SEQUENCE
                                                                                                           SEQUENCE FROM N.A. STRAIN-C3H;
                                                                                                                                                                                                                      CMKBR9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gallus gallus (Chicken).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. MEDLINE; 98244380.
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                                                                                                                                                                                                                                                                                                                                                                                                                      THCCLNPIIYAFIGVKFRNDFFRILHELGCISQETLQEILEVTRKGCGIESDNTTSIST
                                                                                                                                                                                                                                                                                                                                                                                                                                                        FHCCLNPILYAFLGAKFKTS----AQHALTSVSRGSSLKILSKGKRG-GHSSVSTESESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QRQKAVRVAILVTGVFLLCWSPYHIVIFLNTLTKLEAFAKDCLLEDHLDTAIMVTEAIGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DESNRSIC--YFPEAGIHGNNVWLAT-RFLYHSVGFFMPLLVMCYCYMAIVRTLCQSQRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FYLHEHAAGLHRVDRYLAIVYAIHTYRKARARSIHLTCTAIWLSSLLLTLPDLIFMEVWT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QKRKALKTTVILILAFFACWLPYYIGISIDSFILLEIIKQGCEFENTVHKWISITEALAF 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EADDRYICDRFYP-----NDLWVVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LVILERFKRSRTTTENFLFHLTLANLALLLTFPFSVVESLAGWVFGTFLCKILSAVHKIN 155
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 378
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 ΑĀ,
7tm_1; 1.
AA; 43255
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                                                                    PRAGNELL I.B., GRAHAM G.J.;
he EMBL/GenBank/DDBJ databases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 544; DB
Pred. No. 2.8e
B3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Last sequence update)
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Best Local S
Matches 114
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE-SPLEEN;
MARGULIES B.J., HAUER D.A., CLEMENTS J.E.;
"Identification and characterization of thirteen rhesus chemokine receptors and chemokine receptor homologues.";
Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AF100205; AAC72403.1;
Receptor.
SEQUENCE 356 AA; 41210 MW; 30432E9D CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Macaca mulatta (Rhesus macaque).
Eukaryota; Metazoa; Chordata; Craniata; Vertebra;
Eutheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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     243
                                                         183
                                                                                                                                                             123
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                                                                                                                                                          FITLMSVDRYLAVVHAVYAIKVRTIRMGTTTLSLLVWLTAIMATIPLLVFYQVASEDGVL
                                                   QCYSFYNQQTLKWKIFTNFEMNILGLLIPFTIFMFCYIKILHQLKRCQNHNKTKAIRLVL
                                                                                                                                                                                                                                                               CKKLRNITDIYLLNLALSDLLFVFSFPFQTYYQLDQWVFGTVMCKVVSGFYYIGFYSSMF
                                                                                                                                                                                                                                                                                          OKKLRSMTDKYRLHLSVADLLEVITLPEWAVDAVANWYFGNFLCKAVHVIYTVNLYSSVL 125
                                                                                                                                                                                                                                                                                                                                                                                                                       YTSDNYTEEMGSGDY-DSMKEPCFREENANFNKIFLPTIYSIIFLTGIVGNGLVILVMGY
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ILILAFFACWLPYYIGISIDSFILLEIIKQGCEFENTVHKWISITEALAFFHCCLNPILY
                                                                                                 ICDRFYPNDL--WVVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKALKTTV
                                                                                                                                                                                                         ILAFISLDRYLAIVHATNSQRPRKL-LAEKVVYVGVWIPALLLTIPDFIFANVSEADDRY
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114; Conserv
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 528; DB 6;
Pred. No. 4.8e-35;
5; Mismatches 153
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thecidae; Cercopithecinae;
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Best L
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Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata;
Eutheria; Rodentia; Sciurognathi; Murida
                   Eukaryota;
Rodentia;
                             Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
                                                    CMKBR
                                                                        01-JUN-1998
01-MAY-1999
                                                                                                                    055193
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Submitted (MAR-1997) to th
EMBL; U92803; AAB61572.1;
PFAM; PF00001; 7tm_1; 1.
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01-JUL-1997 (TrEMBLrel.
01-NOV-1998 (TrEMBLrel.
SEQUENCE FROM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CCR10-RELATED RECEPTOR.
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                                                             JUN-1998 (TIEMBLIEL. 06,
JUN-1998 (TIEMBLIEL. 06,
MAY-1999 (TIEMBLIEL. 10,
CHEMOKINE RECEPTOR TYPE
                                                                                                                                                                       G----RALRMAAALVVVFFLLMFPYNLTLFLHSLLDLHVF-GNCKISHRLDYMLQVTESL
                                                                                                                                                                                                                                                                                                                                                                                             GSSIY-----DYDYLDDVTVLVCSKDEVLSFGRVFLPVVYSLIFVLGLAGNLL 65
                                                                                                                                                                                                                                                                                                                                                                                                                GISIYTSDNYTEEMGSGDYDSMKE----PCFREENANFNKIFLPTIYSIIFLTGIVGNGL
                                                                                                                                                                                                                                        GHQKRKALKTTVILILAFFACWLPYYIGISIDSFILLEIIKQGCEFENTVHKWISITEAL
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                  Sciurognathi;
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08,
                   Muridae;
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                                                           Created)
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E 2 (C-C CKR-2) (CC-CKR-
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Last annotation updat
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 526.5; DB 1
Pred. No. 6.8e-35;
0; Mismatches 131
                             Vertebrata;
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                   Murinae;
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Muridae; Murinae;
                                                             nnotation update) CKR-2) (CC-CKR-2)
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Rattus.
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Rattus.
                             Eutheria
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Best Local Similarity
Matches 107; Conserv
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DOMAIN
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SEQUENCE
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DOMAIN
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DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                allergic encephalomyelitis.";
J. Neuroimmunol. 86:1-12(1998).
-!- FUNCTION: RECEPTOR FOR THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-SPRAGUE DAWLEY;
MEDLINE; 98318173.
JIANG Y., SALAFRANCA M.N., AL
DEFIEBRE C.M., PENNELL N.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS00237; G_PROTEIN_RECEPTOR; 1. PFAM; PF00001; 7tm_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 JIANG Y., SALAFRANCA M.N., ADHIKARI S., XIA Y., FENG L., SONNTAG M.K., DEFIEBRE C.M., PENNELL N.A., STREIT W.J., HARRISON J.K.; "Chemokine receptor expression in cultured glia and rat experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TRANSMEM
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320
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FUNCTION: RECEPTOR FOR THE MCP-1 (JE), MCP-3 (FIC) AND MCP-5 CHEMOKINES. TRANSDUCES A SIGNAL BY INCREASING THE INTRACELLULAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INDUCTION: IN ANIMALS IN WHICH EXPERIMENTAL ALLERGIC ENCEPHALOMYELITIS (EAE) HAS BEEN INDUCED.
SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CHEMOKINES. TRANSDUCES A SIGNAL BY CALCIUM IONS LEVEL (BY SIMILARITY)
            FLGAKFK 310
                                                                                                                FYPNDLWVVVFQFQHIM---VGLILPGIVILSCYCIIISKLSHSKGHQKR-KALKTTVIL::| :| | | | : :| :|:: :
                                                                                                                                                    LLTIDRYLAIVHAVFALKARTVTFGVITSVVTWVVAVFASLPGIIFTKSEQEDDQHTCGP 205
                                                                                                                                                                     FISLDRYLAIVHATNSQRPRKLLAEKVVYVGVWIPALLLTIPDFIFANVSBADDRYICDR 188
                                                                                                                                                                                                                            LRSMTDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNLYSSVLILA 128
                                                                                                                                                                                                                                                                                   EEMGSG-----DYDSMKEPCFREENANFNKIFLPTIYSIIFLTGIVGNGLVILVMGYQKK 68
FVGEKFR 326
                                                MIVYFLFWTPYNIVLFLTTF - - QEFLGMSNCVVDMHLDQAMQVTETLGMTHCCVNPIIYA 319
                                                                        ILAFFACWLPYYIGISIDSFILLEII-KQGCEFENTVHKWISITEALAFFHCCLNPILYA 303
                                                                                                   YFPT-IWK---NFQTIMRNILSLILPLLVMVICYSGILHTLFRCRNEKKRHRAVRLIFAI 261
                                                                                                                                                                                                        LKSMTDIYLFNLAISDLLELLTLPFWAHYAANEWVFGNIMCKLFTGLYHIGYFGGIFFII 145
                                                                                                                                                                                                                                                           QELDEGATTPYDYDD-GEPCHKTSVKQIGAWILPPLYSLVFIFGFVGNMLVIIILISCKK 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       coupled
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373
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POTENTIAL.
CYTOPLASMIC (POTENTIAL).
BY SIMILARITY.
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CYTOPLASMIC (POTENTIAL).
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14578A08 CRC32;
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Search completed: September 14, 1999, 09:51:50 Job time: 48 sec

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CCR4_BOVIN
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BLR1_MOUSE
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BLR1_HUMAN
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MOMURA H., NIELSEN B.W., MATSUSHIMA K.;

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MEDLINE; 93315164.
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SPECIES-HUMAN; TISSUE-LEUKOCYTE;
MEDLINE; 94103215.
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human homologue, confers neither NPY binding sites nor NPY
responsiveness on transfected cells.";
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SPECIES-HUMAN; TISSUE-BRAIN;
MEDLINE; 94052833.
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OBERLIN E., AMARA A., BACHELERIE F., BESSIA C., VIRELIZIER J.-L.,
ARENZANA-SEISDEDOS F., SCHWARTZ O., HEARD J.-M., CLARK-LEWIS I.,
LEGLER D.F., LOETSCHER M., BAGGIOLINI M., MOSER B.;

"The CXC chemokine SDF-1 is the ligand for LESTR/fusin and prevents infection by T-cell-line-adapted HIV-1.";
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ARENZANA-SEISDEDOS F., SCI
LEGLER D.F., LOETSCHER M.
NATURE 384:288-288(1996).
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L; M99293; G292517; -.
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                                  GCR_0438;
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C-X-C CHEMOKINE REC
                     BENTON P.A., TIMANUS D.K., SHEARER M.H., LEE D.R., KENNE SUBMITTED (NOV-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
-!- FUNCTION: RECEPTOR FOR THE C-X-C CHEMOKINE SDF-1. THE SIGNAL BY INCREASING THE INTRACELLULAR CALCIUM IONS
-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
-!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED
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15-JUL-1998 (REL. 36, LAST SEQUENCE UPDAT
15-DEC-1998 (REL. 37, LAST ANNOTATION UPD
C-X-C CHEMOKINE RECEPTOR TYPE 4 (CXC-R4)
(STROMAL CELL-DERIVED FACTOR 1 RECEPTOR)
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  MACACA FASCICULARIS EUKARYOTA; METAZOA;
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SUBMITTED (JUL-1996) TO EMBL/GENBANK/DDBJ DATA BANK
-!- FUNCTION: RECEPTOR FOR THE C-X-C CHEMOKINE SDF-
SIGNAL BY INCREASING THE INTRACELLULAR CALCIUM
-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN
CONTRACTOR OF THE CONTRACT OF THE CONTRAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIMATES; [1]
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PROSITE; PS00237; G_PROTEIN_RECEPTOR;
PFAM; PF00001; 7tm_1; 1.
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                    LYAFLGAKFKTSAQHALTSVSRGSSLKILSKGKRGGHSSVSTESESSSFHSS
                                                                           TVILILAFFACWLPYYIGISIDSFILLEIIKQGCEFENTVHKWISITEALGFFHCCLNPI
                                                                                            TVILILAFFACWLPYYIGISIDSFILLEIIKQGCEFENTVHKWISITEALAFFHCCLNPI
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                                                                                                                                                                           DDRYICDRFYPNDLWVVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKALKT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 (POTENTIAL).

2 (POTENTIAL).

3 (POTENTIAL).

4 (POTENTIAL).

4 (POTENTIAL).

EXTRACELLULAR (POTENTIAL).

5 (POTENTIAL).

5 (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

6 (POTENTIAL).

EXTRACELLULAR (POTENTIAL).

7 (POTENTIAL).
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Pred. No. 7.6e
5; Mismatches
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BY SIMILARITY.
N; 7EDA93BA CRC32;
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CYTOPLASMIC (P
2 (POTENTIAL).
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.6e-116;
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Subspecies or clinical evolution.";
AIDS RES. HUM. RETROVIRUSES 14:639-641(1998).
-!- FUNCTION: RECEPTOR FOR THE C-X-C CHEMOKINE SDF-1. TRANSDUCES A SIGNAL BY INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL.
-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
-!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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15-JUL-1998 (REL. 36, CREATED)
15-JUL-1998 (REL. 36, LAST SEQUENCE UPDATE)
15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
C-X-C CHEMOKINE RECEPTOR TYPE 4 (CXC-R4) (CXC
(STROMAL CELL-DERIVED FACTOR 1 RECEPTOR) (FUS
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CCR4_MACMU
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TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EDINGER A.L. AMEDEE A., MILLER K., DORANZ B.J., ENDRES M., SHARRON M., SAMSON M., LU Z.-H., CLEMENTS J.E., MURPHEY-CORB M., PEIPER S.C., PARMENTIER M., BRODER C.C., DOMS R.W.; "Differential utilization of CCR5 by macrophage and T cell tropic simian immunodeficiency virus strains."; PROC. NATL. ACAD. SCI. U.S.A. 94:4005-4010(1997).
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MEDLINE; 97213934.
CHEN Z., ZHOU P., HO D.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MACACA MULATTA (RHESUS MACAQUE).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUT
PRIMATES; CATARRHINI; CERCOPITHECIDAE; CERCOPITHECINAE;
                                                                                                                                                                                                                                                                                                                   entities requires a license agreement (S or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Generically divergent strains of "Genetically divergent strains of CCR5 as a coreceptor for entry."; VIROL. 71:2705-2714(1997).
                                                                  TRANSMEM
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U93311; G1934671; -.
AF001928; G2911294; .
; GCR_1297; -.
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EXTRACELLULAR (
5 (POTENTIAL).
CYTOPLASMIC (PO
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EXTRACELLULAR (
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CYTOPLASMIC (PO
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Best Local
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062747;
15-DEC-1998 (
15-DEC-1998 (
15-DEC-1998 (
                                                                                                                              SEQUENCE FROM N.A.

MEDILINE; 98321155.

CHEN Z., GETTIE A., HO D.D., MARX P.A.;

Primary SIVsm isolates use the CCR5 coreceptor from sooty mangabey naturally infected in west Africa: a comparison of coreceptor usage of primary SIVsm, HIV-2, and SIVmac.";

VIROLOGY 246:113-124(1998).

-1- FUNCTION: RECEPTOR FOR THE C-X-C CHEMOKINE SDF-1. TRANSDUCES A SIGNAL BY INCREASING THE INTEGRAL MEMBRANE PROTEIN.

-1- SUBCELULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.

-1- SUBCELULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
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DISULFID
CONFLICT
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CONFLICT
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                                  use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                               This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the El the European Bioinformatics Institute. There are no resti
                                                                                                                                                                                                                                                                                                                               C-X-C CHEMOKINE RECEPTOR TYPE 4 (CXC-R4) (CXCR-4) (SDF-1 RECEPTOR) (STROMAL CELL-DERIVED FACTOR 1 RECEPTOR) (FUSIN) (LESTR).
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EMBL; AF051906; G3135304; PROSITE; PS00237; G_PROTE

G_PROTEIN_RECEPTOR;

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RESULT 6
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Best Local Similarity
Matches 344; Conser
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CCR4_FELCA STANDARD;
CCR4_FELCA STANDARD;
P56498; P79172; O02700;
15-JUL-1998 (REL 36, CREATED)
15-JUL-1998 (REL 36, LAST SEQUENCE UPDATE)
15-JUL-1998 (REL 36, LAST ANNOTATION UPDATE)
15-JUL-1998 (REL 36, LAST ANNOTATION UPDATE)
C-X-C CHEMOKINE RECEPTOR TYPE 4 (CXC-R4) (CXCR-4)
C-X-C CHEMOKINE RECEPTOR TYPE 4 (CXC-R4) (FUSIN) (FUSIN)
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DISULFID
SEQUENCE
[2]
SEQUENCE
                                                             SEQUENCE;
                                                                                       FELIS SILVESTRIS CATUS (CAT). V
EUKARYOTA; METAZOA; CHORDATA; V
CARNIVORA; FISSIPEDIA; FELIDAE;
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                                  "Shared
                                            WILLETT B.J.,
CLAPHAM P.R.;
                "Shared usage of the chemokine immunodeficiency viruses.";
J. VIROL. 71:6407-6415(1997).
                                                                                                                      CXCR4
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1 (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

2 (POTENTIAL).

2 (POTENTIAL).

5 (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

6 (POTENTIAL).
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6 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
7 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
POTENTIAL.
BY SIMILARITY.
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Pred. No. 4.2e
7; Mismatches
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                                                                                         VERTEBRATA; MAMMALIA;
E; FELIS.
                                                    M.J.,
                                   receptor CXCR4
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SUBMITTED (MAR-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
SUBMITTED (MAR-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
-i- FUNCTION: RECEPTOR FOR THE C-X-C CHEMOKINE SDF-1. TRANSDUCES A
SIGNAL BY INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL.
-i- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
-i- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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GCRDB; GCR_1114;
PROSITE; PS00237;
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EMBL; U92795;
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SUBMITTED (DE
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                                                                                                    ILYAFLGAKFKTSAQHALTSVSRGSSLKILSKGKRGGHSSVSTESESSSFHSS
                              TTVILILAFFACWLPYYIGISIDSFILLEIIKQGCEFENTVHKWISITEALAFFHCCLNP
                                                                       ADDRYICDREYPNDLWVVVEQEQHIMVGLILFGIVILSCYCIIISKLSHSKGHQKRKALK
                    TTVILILAFFACWLPYYIGISIDSFILLEIIKQGCEFESTVHKWISITEALAFFHCCLNP
                                                             ADGRYICDRFYPSDSWLVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGYQKRKALK
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94.6%;
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D -> E (IN REF
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Pred. No. 1.8e-111;
l; Mismatches 7;
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CYTOPLASMIC (POTENTIAL).
POTENTIAL.
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REF. 3
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01-MAY-1992 (REL. 22, CREALL, 01-MAY-1992 (REL. 22, LAST SEQUENCE UPDATE)
01-MAY-1992 (REL. 22, LAST SEQUENCE UPDATE)
15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
C-X-C CHEMOKINE RECEPTOR TYPE 4 (CXC-R4) (CXCR-4) (SD
(STROMAL CELL-DERIVED FACTOR 1 RECEPTOR) (FUSIN) (LET)
(STROMAL CELL-DERIVED FACTOR 1 RECEPTOR) (LESTR) (LCR1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE; 940
JAZIN E.E.,
SALON J., LA
CARBOHYD
DISULFID
SEQUENCE
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DOMAIN
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                                                                                                                                                                                                                                                   PIR;
                                                                                                                                                                                                                                                                                                                                                                                                                       -
                                                                                                                                                                                                                                                                                                                                                                                                                                                    "A proposed bovine neuropeptide Y (NPY) receptor human homologue, confers neither NPY binding site responsiveness on transfected cells."; REGUL. PEPT. 47:247-258(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE; 92:
RIMLAND J.,
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P25930;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Sequence and expression of a neuropeptide Y receptor cDNA.", MOL. PHARMACOL. 40:869-875(1991).
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                                                                                                                                                                                                                                                                                 send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                        FUNCTION: RECEPTOR FOR THE C-X-C CHEMOKINE SDF-1. TRANSDUCES A SIGNAL BY INCRASING THE INTRACELLULAR CALCIUM IONS LEVEL. SUBCELLULAR LOCATION: INVEGRAL MEMBRANE PROTEIN.
TISSUE SPECIFICITY: BRAIN, HEART, KIDNEY, LUNG AND LIVER.
SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS. CAUTION: WAS ORIGINALLY (REF.1) THOUGHT TO BE A RECEPTOR FOR NEUROPEPTIDE Y, TYPE 3 (NPY3-R).
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E; PS00237; G_PROTEIN_RECEPTOR;
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CYTOPLASMIC (POTENTIAL).

4 (POTENTIAL).
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                                                                                                                                                                                                                                                                "Cloning of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P70658; P70346; 009062; 009059; P70233;
01-NOV-1997 (REL. 35, CREATED)
01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
C-X-C CHEMOKINE RECEPTOR TYPE 4 (CXC-R4) (CXCR-4)
(STROMAL CELL-DERIVED FACTOR 1 RECEPTOR) (FUSIN)
SEVEN TRANSMEMBRANE DOMAIN RECEPTOR) (LESTR).
growth-stimulating
murine homolog of t
fusin.";
           TISSUE-BONE MARROW;
MEDLINE; 97121456.
NAGASAWA T., NAKAJIMA T., TACHIBANA K., IIZASA H., BLEUL C.C.,
NAGASAWA T., NAKAJIMA T., YOSHIDA N., SPRINGER T.A., KISHIMOTO
YOSHIE O., MATSUSHIMA K., YOSHIDA N., SPRINGER T.A., KISHIMOTO
"Molecular cloning and characterization of a murine pre-B-cell
growth-stimulating factor/stromal cell-derived factor 1 receptomurine homolog of the human immunodeficiency virus 1 entry core
                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. STRAIN=C57BL/6J;
                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=129/SV;
HEESEN M., BER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MUS MUSCULUS (MOUSE) EUKARYOTA; METAZOA;
                                                                                                                                                                               SEQUENCE FROM N.A
                                                                                                                                                                                                                                           co-factor
                                                                                                                                                                                                                                                                                                               MEDLINE; 97113334.
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O (NOV-1996) T
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                                                                                                                                                                                                                                                                                        BENSON
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Pred. No. 3.4
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KISHIMOTO
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PROSITE; PS00237; G_PROTEIN_RECEPTOR; 1.

PFAM; PF00001; 7tm_1; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entropean Bioinformatics Institute. There are no restructed by non-profit institutions as long as its content
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SUBMITTED (SEP-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
-!- FUNCTION: RECEPTOR FOR THE C.Y-C CHEMOKINE SDF-1. TRANSDUCES A
SIGNAL BY INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL.
-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
-!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   G-PROTEIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-C57BL/6; TISSUE-THYMUS;
SUZUKI G., NAKATA Y., UZAWA A., SHIRASAWA T., SAITO T.,
SUBMITTED (FEB-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
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GYQKKLRSMTDKYRLHLSVADLLEVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNLYSS
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Z80112;
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X99582;
U59760;
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D87747;
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319; Conser
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GCR_1387;
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COUPLED RECEPTOR;
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CYTOPLASMIC (POTENTIAL).
6 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
7 (POTENTIAL).
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Pred. No. 3.3e
19; Mismatches
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EXTRACELLULAR (POTENTIAL)

5 (POTENTIAL)
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I -> V (IN REF. 1 AND; 1037B4D3 CRC32;
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01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
C-X-C CHEMOKINE RECEPTOR TYPE 4 (CXC-R4) (CXCR-4) (SDF-1 RECEPTOR)
(STROMAL CELL-DERIVED FACTOR 1 RECEPTOR) (FUSIN) (LEUKOCYTE-DERIVED
  CARBOHYL
                                                                                                                                           TRANSMEM
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PROSITE; PS00237
PFAM; PF00001; 7
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HARRISON J.K., SALAFRANCA M.N.;
SUBMITTED (MAR-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
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SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                         OVER C.J., MATTERI R.L., KEISLER D.H.;
"Nevelopment of an ovine Y3 cDNA and expression of the Y3 receptor mRNA in the ovine hypothalamus and pituitary.";
ABSTR. - SOC. NEUROSCI. 21:1890-1890(1995).
-!- FUNCTION: RECEPTOR FOR THE C-X-C CHEMOKINE SDF-1. TRANSDUCES A SIGNAL BY INCRESSING THE INTRECLIQUAR CALCIUM IONS LEVEL.
-!- SUBCELJULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
-!- SUBCELJULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
-!- SUBCELJULAR LOCATION: INTEGRAL MEMBRANE PROTEIN COUPLED RECEPTORS.
-!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTIORS.
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15-JUL-1998 (REL. 36, CREATED)

15-JUL-1998 (REL. 36, LAST SEQUENCE UPDATE)

15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)

15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)

C-X-C CHEMOKINE RECEPTOR TYPE 4 (CXC-R4) (CXCR-4) (SDF-1 RECEPTOR)

(STROWAL CELL-DERIVED FACTOR 1 RECEPTOR) (FUSIN) (LEUKOCYTE-DERIVED
  GCRDB; GCR_1581;
PROSITE: PS00237; G_PROTEIN_RECEPTOR;
PFAM; PF00001; 7tm_1; 1.
G-PROTEIN COUPLED RECEPTOR; TRANSMEMB
                                                                                                                                                                                                                   the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                  EMBL; U38942;
                                                                                                                                                                  or send an email to license@isb-sib.ch).
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ORA; BOVOIDEA; BOVIDAE; CAPRINAE;
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              IMAIT., BABA M., NISHINURA M., KAKIZAKI M., TAKAGI S., YO
IMAIT., BABA M., NISHINURA M., KAKIZAKI M., TAKAGI S., YO
"The T cell-directed CC chemokine TARC is a highly specific biological ligand for CC chemokine receptor 4.";
J. BIOL. CHEM. 272:15036-15042(1997).
-!- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO SUBSEQUENTLY TRANSDUCES A SIGNAL BY INCREASING THE INTOCALCIUM IONS LEVEL.
-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
-!- TISSUE SPECIFICITY: EXPRESSED STRONGLY IN PERIPHERAL E BUT NOT IN B CELLS, NATURAL KILLER CELLS, MONOCYTES, CRANULOCYTES.
                                                                                                                                                                                                                                    MEDLINE; 953/040-1.
MEDLINE; 953/040-1.
POWER C.A., MEYER A., NEMLL.;
PROUDFOOT A.E.I., WEILS T.N.C.;
"Molecular cloning and functional expression of a receptor cDNA from a human basophilic cell line."
T BIOL. CHEM. 270:19495-19500(1995).
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; METAZOA; CHORDATA; VERT
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(REL: 34, LAST SEQUENCE UPDATE)
(REL. 37, LAST ANNOTATION UPDATE)
NE RECEPTOR TYPE 4 (C-C CKR-4) (CC-CKR-4) (CCR-4) (CCR4)
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L3; Mismatches
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EUKARYOTA; METAZOA; CHOF
RODENTIA; SCIUROGNATHI;
                                 RECEPTOR).
ILBRB OR CXCR2
                                                          HIGH AFFINITY
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GCRDB; GCR_211
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ween the Swiss Institute of Bioinformatics and the EMBL outst
European Bioinformatics Institute. There are no restrictions
by non-profit institutions as long as its content is in
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33, LAST SEQUENCE UPDATE)
36, LAST ANNOTATION UPDATE)
36, LAST ANNOTATION B (IL-8R
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            CHORDATA;
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39.7%;
NDATA; VERTEBRATA;
MURIDAE; MURINAE;
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Pred. No. 3.1e
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No. 3.1e-34;
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MAMMALIA;
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Query Match Best Local Similarity

31.8%; 36.6%;

Score 581.5; DB 1;
Pred. No. 6.1e-33;

Length 359;

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SUBMITTED (FEB-1994) 10 [2]
[2]
SEQUENCE FROM N.A.
STRAIN-WISTAR; TISSUE-LIVER;
STRAIN-WISTAR; SHIBATA F., WATAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   [1]
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN-SPRAGUE-DAWLEY; T
GOBL A.E., WANG S., ZHOU
SUBMITTED (FEB-1994) TO
CARBOHYD
CARBOHYD
DISULFID
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Identification of two rat genes orthologous to the human interleukin-8 receptors.";
J. BIOL. CHEM. 271:32770-32776(1996).
-i. FUNCTION: RECEPTOR TO INTERLEUKIN-8, WHICH IS A POWERFUL NEUTROPHILS CHEMOTACTIC FACTOR. BINDING OF IL-8 TO THE RECEPTOR CAUSES ACTIVATION OF NEUTROPHILS. THIS RESPONSE IS MEDIATED VIA A G-PROTEIN THAT ACTIVATE A PHOSPHATIDYLINOSITOL-CALCIUM SECOND MESSENGER SYSTEM. THIS RECEPTOR BINDS TO IL-8 WITH A HIGH AFFINITY AND TO GRO/MGSA AND NAP-2 ALSO WITH A HIGH AFFINITY.
-i. SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN COUPLED RECEPTORS.
                                                                             TRANSMEM
DOMAIN
TRANSMEM
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CARBOHYD
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TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KONISHI
FUJIOKA
                                             CARBOHYD
                                                                                                                                              TRANSMEM
                                                                                                                                                                                                                                      CHEMOTAXIS
                                                                                                                                                                                                                                                           PROSITE; PS002:
PFAM; PF00001;
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GCRDB; GCR_1405;
GCRDB; GCR_1524;
                                                                                                                                                                                                                                                                                                                  EMBL; X77797; G498703; -. EMBL; D63584; G944819; -. EMBL; U70988; G1617613; -EMBL; S42096; S42096.
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                                                                  N.A.
;; TISSUE-SPLEEN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SALAFRANCA M.N., ADHIKARI S.,
                                                                                                                                                                                                                                                                       G_PROTEIN_RECEPTOR;
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                              7 (POTENTIAL).
CYTOPLASMIC (F
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2 (POTENTIAL).
EXTRACELLULAR
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BY SIMILARITY
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7 (POTENTIAL).
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6 (POTENTIA:
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 CRC32;
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01-FEB-1996 (REL. 33, CREATED)

01-NOV-1997 (REL. 35, LAST SEQUI

15-JUL-1998 (REL. 36, LAST ANNO)

C-X-C CHEMOKINE RECEPTOR TYPE 3

CXCR3 OR GPR9.

HOMO SAPIENS (HUMAN).

EUKARYOTA; METAZOA; CHORDATA; VI
                                                                                                                                                                                                                                                                                         LOETSCHER M., GERBER B., LOETSCHER P., JONES S.A., PIALI L
CLARK-LEWIS I., BAGGIOLINI M., MOSER B.;
"Chemokine receptor specific for IP10 and mig: structure,
and expression in activated T-lymphocytes.";
J. EXP. MED. 184:963-969(1996).
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                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                    and GPR14, encoding receptors related to Y, and somatostatin receptors.";
                                                                                                                                                                                                               MARCHESE A., HEIBER M., NGUYEN T., CHENG R., MURPHY P.M., TSUI L.-C., O'DOWD B.F., DOCHERTY J.M.;
                                                                                                                                                                                                                                       MARCHESE A., HEIBER M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CCR3
                                                          the
                                                                                                                                                          GENOMICS 29:335-344(1995)
                                                                                                                                                                                                                                                        SEQUENCE OF 5-368 FROM N.A. MEDLINE; 96115583.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HUMAN
                                                                                                                                                                                   "Cloning and chromosomal mapping of three novel genes, (and GPR14, encoding receptors related to interleukin 8,
                                                                                                                                                                                                                                                                                                                                                                          MEDLINE;
                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A
                                                                                                            -:- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
-:- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS
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European Bioinformatics Institute.
                                                                                                                                           FUNCTION: RECEPTOR FOR IP10 AND MIG.
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35, LAST SEQUENCE UPDATE)
36, LAST ANNOTATION UPDATE)
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                                                                                                                                                                                                                                                                                                                                                                                                                             VERTEBRATA; MAMMALIA; AE; HOMO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 (CXC-R3) (CXCR-3).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          368
              (See http://www.isb-sib.ch/announce,
                                                         There
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                                       as its content
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                             Usage
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                             by and for
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                                                       restrictions
                                                                                                                                                                                                GPR9, GPR10
                                                                                                                                                                                   neuropeptide
                                                                                                                                                                                                                                                                                                                            function,
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ROCOSCIDITA
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Best Local S
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                                    P25025;
01-MAY-1992 (REL. 22, CREATED)
01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
15-JUL-1998 (REL. 36, LAST ANNOTATION UPDAT
HIGH AFFINITY INTERLEUKIN-8 RECEPTOR B (IL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; X95876; E22393
EMBL; U32674; G10027
GCRDB; GCR_1341; -.
GCRDB; GCR_1972; -.
                                                                                                                                                                                                                                                                                                                                                                                                                   CARBOHYD
SEQUENCE
                                                                                        IL8B_HU
P25025;
      IL8RB OR CXCR2.
HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CI
PRIMATES; CATARRHINI;
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DISULFID
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                                                                                                                                               FVGVKFRERMWMLL-----
                                                                                                                                                                                           LILAFFACWLPYYIGISIDSFILLEIIKQGCEFENTVHKWISITEALAFFHCCLNPILYA 303
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          600894;
                                                                                                   HUMAN
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                                                                                                                                                                                 VVVAFALCWTPYHLVVLVDILMDLGALARNCGRESRVDVAKSVTSGLGYMHCCLNPLLYA
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                                                                                                  STANDARD;
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110
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1147
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1203
               CHORDATA; VERTEBRATA; MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                                                                                    40659
                                                                                                                                                                                                                                                                                                                                                                               31.5%;
        HOMINIDAE;
                                                                                                                                               ---LRLGCPNQRGLQRQPSSSRRDSSW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               6 (POTENTIAL).

EXTRACELLULAR (POTENTIAL)

7 (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                             Score 576.5;
Pred. No. 1.
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BY SIMILARITY.
POTENTIAL.
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6 (POTENTIAL
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3 (POTENTIAL)
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2 (POTENTIA
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1 (POTENTIAL)
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B (IL-8R
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.4e-32;
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                                                    (CXCR-2)
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                EUTHERIA;
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                                                    (GRO/MGSA
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GCRDB; GCR_0077; -.
GCRDB; GCR_0610; -.
GCRDB; GCR_1001; -.
GCRDB; GCR_1339; -.
GCRDB; GCR_1831; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE; 91368200.
MURPHY P.M., TIFFANY H.L.;
"Cloning of complementary DNA ei
interleukin-8 receptor.";
SCIENCE 253:1280-1283(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                    entities
or send a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        J. BIOL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  between the Swiss Institute of Bioinformat the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE;
                                                         PROSITE: PS00237; G_PROTEIN_RECEPTOR: PFAM: PF00001; 7tm_1; 1. HSSP: P34996; 1DDD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. MEDLINE; 94209273. SPRENGER H., LLOYI
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                                                                                                                                                                                                                                                          PIR; A39446; A39446.
PIR; A53611; A53611.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A., AND CHARACTERIZATION MEDLINE: 93205012.
CERRETTI D.P., KOZLOSKY C.J., VANDEN BOS BECKMANN M.P.;
                                         G-PROTEIN COUPLED RECEPTOR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 receptors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AHUJA S.K., SHETTY A., TIFFANY H.L., MURPHY "Comparison of the genomic organization and human interleukin-8 receptors A and B."; J. BIOL. CHEM. 269:26381-26389(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GRO/melanoma growth-stimulatory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Characterization of tw
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=PLACENTA;
MEDLINE; 95014476.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SPRENGER H., LLOYD A.R., LAUTENS L.L., BONNER T.I., "Structure, genomic organization, and expression of interleukin-8 receptor B gene.", BIOL. CHEM. 269:11065-11072(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Molecular characterization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FUNCTION: RECEPTOR TO INTERLEUKÍN-8, WHICH IS A POWERFUL NEUTROPHILS CHEMOTACTIC FACTOR. BINDING OF IL-8 TO THE RECEPTOR CAUSES ACTIVATION OF NEUTROPHILS. THIS RESPONSE IS MEDIATED VIA A G-PROTEIN THAT ACTIVATE A PHOSPHATIDYLINOSITOL-CALCIUM SECOND MESSENGER SYSTEM. THIS RECEPTOR BINDS TO IL-8 WITH A HIGH AFFINITY AND TO GRO/MGSA AND NAP-2 ALSO WITH A HIGH AFFINITY. SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.

SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                                                                                                                                                                                                                   L; M73969; G1109691; -.

L; M94582; G186378; -.

L; M99412; G576679; -.

L; L19593; G559054; -.

L; U11869; G511803; -.
                                                                                                                                146928
                                                                                                                                                                                                                                                                                                                                                                                                                               s requires a license agreement (See http://www.isb-sib.ch/announce/an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; 92355587.
HORUK R.,
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48
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                                       TRANSMEMBRANE;
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                                       GLYCOPROTEIN;
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promoter
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Q1-NOV-1997
Q1-NOV-1997
Q1-NOV-1997
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DISULFID
SEQUENCE
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EUKARYOTA; METAZOA; CHORDATA; V
                                                                                                                            HIGH AFFINITY INTERLEUKIN-8 IL8RB OR CXCR2.
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"Characterization of interleukin-8 receptors IMMUNOGENETICS 43:261-267(1996).
-i-FUNCTION: RECEPTOR TO INTERLEUKIN-8, WHI NEUTROPHILS CHEMOTACTIC FACTOR. BINDING
                                                      MEDLINE; 96
ALVAREZ V.,
                                                                          SEQUENCE
                                            LOPEZ - LARREA
                                                                                               PRIMATES;
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                                          FROM N., 96175151.
COTO F
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(REL. 35, LAST ANNOTATION
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                               non-human primates.";
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                                                                                                         EUTHERIA;
  THE RECEPTOR
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CAUSES ACTIVATION OF NEUTROPHILS, THIS RESPONSE IS MEDIATED VIA A G-PROTEIN THAT ACTIVATE A PHOSPHATIDIVINOSITOL-CALCIDM SECOND MESSENCER SYSTEM. THIS RECEPTOR BINDS TO IL-8 WITH A HIGH AFFINITY AND TO GRO/MGSA AND NAP-2 ALSO WITH A HIGH AFFINITY.

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Query Match 31.0%;
Best Local Similarity 37.0%;
Matches 127; Conservative 6/
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS00237; G_PROTEIN_RECEPTOR; 1.
PFAM; PF00001; 7tm_1; 1.
HSSP; P34996; 1DDD.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                                                                                                                                                              FALTLPIWAASKVNGWIFGTFLCKVVSLLKEVNFYSGILLLACISVDRYLAIVHATRTLT 153
                              SVSRGSSLKILSKGKRGGHSSVSTES-----
                                                                                      ISIDSFILLEIIKQGCEFENTVHKWISITEALAFFHCCLNPILYAFLGAKFKTSAQHALT
                                                                                                                      LRILPQSFGFIVPLLIMLFCYGFTLRTLFKAHMGQKHRAMRVIFAVVLIFLLCWLPYSLV
                                                                                                                                                                                    QKRYLV-KFICLSIWGLSLLLALPVLLFRRTVYSSNVSPA----CYEDMGNNTANWRML
                                                                                                                                                                                                                 PRKLLAEKVVYVGVWIPALLLTIPDFIF-----ANVSEADDRYICDRFYPNDL--WVVV
                                                                                                                                                                                                                                                                            FVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNLYSSVLILAFISLDRYLAIVHATNSQR 146
                                                                                                                                                                                                                                                                                                          PC-RPESLEINKYEVVIIYALVELLSLIGNSLVMLVILYSRVGRSVTDVYLLNLALADLL
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                                                           LLADTLMRTQVIQETCERRNHIDRALDATEILGILHSCLNPLIYAFIGQKFR---
                                                                                                                                                    FQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKALKTTVILILAFFACWLPYYIG
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39947 MW;
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5 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
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EXTRACELLULAR (POTENTIAL).
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1 (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

2 (POTENTIAL).
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CYTOPLASMIC (
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3 (POTENTIAL).
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Query Match
Best Local Similarity
Matches 352; Conserv

100.0%; Score 1830; DB 2; ilarity 100.0%; Pred. No. 4.6e-143; Conservative 0; Mismatches 0;

Length 352; Indels 0

0; Gaps

A. Molecule type: mRNA A. Residues; 1-32 < FEDD RICOSS references GB: M99293; NTD: 9282515; PTD: 9292517 RICOSTSCHEER, GB: M99293; NTD: 9282516; PTD: 9292517 RICOSTSCHEER, GB: M99293; NTD: 92816; RI: Baggiolini, M.; Moser, B. J. Biol. Chem. 269, 232-237, 1994 A. Title: Cloning of a human seven transmembrane domain receptor, LESTR, that is highl A. Residues in 132 CADD A. Reference number: A53103; MNID: 9410215 A. A. Residues; 1-322 CADD A. Molecules; 1-322 CADD A. Cross references; BMBL: X1635; NID: 9297099; PID: 9297100 R. Herzoy, B.; Hort (12.7); Shine, J.; Selbie, L.A. DIN (cell Biol. 12. 46-471, 1993 A. Fille: Molecular cloning, Characterization, and localization of the human homolog to the following the following the following translated from GB/EMBL/DDBJ A. Residues; 1-322 CABD A. Residues; 1-322 CABD A. Cross references: GB: L06797; NID: 9414929; PID: 9414928; A. Residues; 1-322 CABD A. Residues; 1-322 CABD A. Residues; 1-324 CABD A. Residues; 1-352 CABD A. Residues; 1	25.9 359 2 139418 angiotensin II 25.9 362 2 A30341 G protein-coupl 25.8 359 2 JC1193 angiotensin II 25.8 359 2 JC1194 angiotensin II 25.8 359 2 JC1194 ALIGNMENTS ALIGNMENTS	481 26.3 359 2 480.5 26.3 359 2
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submitted to GenBank, July
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A:Molecule type: mRNA
A:Residus: 1-352 <TAT>
A:Cross-references: GB:D86579; NID:g1468948; PID:g1468949
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346; Conser
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Pred. No. 4
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C; Species:

neuropeptide Y/peptide YY receptor C;Species: Bos primigenius taurus (

(cattle)

У3 -

bovine

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A;Cross-references: GDB:677463
A;Aryap position: 3p21-3p21
C;Keywords: G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane F;40-65/Domain: transmembrane #status predicted <TM1>
F;40-65/Domain: transmembrane #status predicted <TM2>
F;112-13/Domain: transmembrane #status predicted <TM3>
F;112-13/Domain: transmembrane #status predicted <TM4>
F;51-175/Domain: transmembrane #status predicted <TM6>
F;208-226/Domain: transmembrane #status predicted <TM6>
F;243-264/Domain: transmembrane #status predicted <TM6>
F;243-264/Domain: transmembrane #status predicted <TM6>
F;291-308/Domain: transmembrane #status predicted <TM6>
F;291-308/Domain: transmembrane #status predicted <TM7>
F;291-308/Domain: transmembrane #status predicted <TM7>
F;291-308/Domain: transmembrane #status predicted <TM7>
F;29-276,110-187/Disulfide bonds: #status predicted
F;273,350/Binding site: phosphate (Ser) (covalent) (by casein kinase II) #status pred
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A; Reference number: $28787; MUID:92100053
A; Accession: $28787
A; Molecule type: mRNA
A; Residues: 1-353 < KIMS
A; Cross-references: EMBL:M86739
C; Keywords: appetite; G protein-coupled receptor; transmembrane protein
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A; Gene: GDB: CMKBR4
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A; Residues: 1-360 < POW>
A; Cross-references: GB: X85740;
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A;Accession: A57160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Species: Homo sapiens (man)
C;Date: 10-Nov-1995 #sequence_revision 10-Nov-1995 #text_change 17-Mar-1999
C;Accession: A57160
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                                                                                                                                                                                                                                                                                                                                                                         A; Note: source clone
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Pred. No. 3.1e-134;
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interferon-inducible protein 10 (IP-10) receptor - mouse (.Species: Mus musculus (house mouse) C;Date: 05-Feb-1999 #sequence_revision 05-Feb-1999 #text_change C;Accession: JE0349  
R;Tamaru, M.; Tominaga, Y.; Yatsunami, K.; Narumi, S. Biochem. Biophys. Res. Commun. 251, 41-48, 1998 A;Title: Cloning of the murine interferon-inducible protein 10 (A;Reference number: JE0349 A;Accession: JE0349
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C;Comment: This protein is import
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A; Residues: 1-367 < TAM>
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KTSAQHALTSVSRGSSLKILSKGKRGGHSSVSTESESSSF 349
                                                                                                                               FP-QVGRTALRVLQLVAGFLLPLLVMAYCYAHILAVLLVSRGQRRFRAMRLVVVVVAAFA
                                                                                                                                                                  YPNDLWVVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKALKTTVILILAFF 249
                                                                                                                                                                                                                                              RYLAIVHATNSQR---PRKLLAEKVVYVGVWIPALLLTIPDFIF--ANVSEADDRYICDRF
                                                                                                                                                                                                                                                                                                       DKYRLHLSVADLLEVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNLYSSVLILAFISLD 133
                                                                                                                                                                                                                                                                                                                                                           DYGENESDFSDSPPCPQDFSLNFDRTFLPALYSLLFLLGLLGNGAVAAVLLSQRTALSST
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                                                       VCWTPYHLVVLVDILMDVGVLARNCGRESHVDVAKSVTSGMGYMHCCLNPLLYAFVGVKF
                                                                                                                                                                                                      RYLSIVHATQIYRRDPRVRVA--LTCIVVWGLCLLFALPDFIYLSANYDQRLNATHCQYN
                                                                                                                                                                                                                                                                                  DTFLLHLAVADVLLVLTLPLWAVDAAVQWVFGPGLCKVAGALFNINFYAGAFLLACISFD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ISIDSFILLEIIKQGCEFENTVHKWISITEALAFFHCCLNPILYAFLGAKFK 310
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                                                                                         ACWLPYYIGISIDSFILLEIIKQGCEFENTVHKWISITEALAFFHCCLNPILYAFLGAKF 309
                                                                                                                                                                                                                                                                                                                                                                                                                                     al Similarity 35.6
121; Conservative
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35.6%;
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Pred. No. 1.2e-40;
0; Mismatches 133;
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Pred. No. 3.7e-42;
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interleukin-8 receptor type B - human (Species: Homo sapiens (man) (C;Species: Homo sapiens (man) (C;Species: Homo sapiens (man) (C;Date: 07-Oct-1994 #sequence_revision 12-Apr-1996 #text_change 29-Aug-1997 (C;Accession: 137898; 138712; A53611; A39446 R;Ahuja, S.K.; Shetty, A.; Tiffany, H.L.; Murphy, P.M. J. Biol. Chem. 269, 26381-26389, 1994 A;Title: Comparison of the genomic organization and promoter function for he A;Reference number: 137898; MUID:95014476 A;Accession: 137898; MUID:95014476
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R;Murphy, P.M.; Tiffany, H.L.
Science 253, 1280-1283, 1911
A;Title: Cloning of complementary DNA encoding a functional human interleukin-8 recep A;Reference number: A39446; MUID:91368200
A;Accession: A39446
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A;Cross·references: GDB:127868; OMIM:146928
A;Map position: 2435-2435
C;Keywords: G protein-coupled receptor; tra
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A; Residues: 6-360 <SPR>
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A;Title: Structure, genomic organization, and expression of the human interleukin: R;Reference number: A;3611; MUID:94209273

A;Accession: A;3611
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A; Residues: 1-15 < RE2>
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A; Residues: 1-360 < RES>
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Best Local
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AHMGQKHRAMRVIFAVVLIFLLCWLPYNLVLLADTLMRTQVIQETCERRNHIDRALDATE
                                              SKGHOKRKALKTTVILILAFFACWLPYYIGISIDSFILLEIIKQGCEFENTVHKWISITE 288
                                                                                              TVYSSNVSPA-----CYEDMGNNTANWRMLLRILPQSFGFIVPLLIMLFCYGFTLRTLFK 240
                                                                                                                                                                                                TVNLYSSVLILAFISLDRYLAIVHATNSQRPRKLLAEKVVYVGVWIPALLLTIPDFIF-- 175
                                                                                                                                                                                                                                                                                                                                                          GLVILVMGYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIY 116
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                                                                                                                                    ----ANVSEADDRYICDRFYPNDL--WVVVFQFQHIMVGLILPGIVILSCYCIIISKLSH
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Pred. No. 1.7e-39;
9; Mismatches 119;
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chemokine (C-C) receptor 4 - mouse (C;Species: Mus musculus (house mouse) (C;Species: Mus musculus (house mouse) (C;Date: 08-Mar-1996 #sequence_revision 19-Apr-1996 #text_change 12-Dec-1997 (C;Accession: JC4587 R;Hoogewerf, A.J.; Black, D.; Proudfoot, A.E.I.; Wells, T.N.C.; Power, C.A. Blochem. Biophys. Res. Commun. 218, 337-343, 1996 A;Title: Molecular cloning of murine CC CKR-4 and high affinity binding of A;Reference number: JC4587 A;Accession: JC4587
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C;Specles: Rattus norvegicus (Norway rat)
C;Date: 06-Jan-1995 #sequence_revision 06
C;Accession: $42096
R;Gobl, A.E.; Wang, S.; Zhou, Y.; Oeberg,
A; Molecule type:
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C;Keywords: G protein-coupled receptor; transmembrane protein
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A; Residues: 1-356 <GOB>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VSEAD-DRYICDREYPN-----DLWVVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSK 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EITFYSSVLLLACISMDRYLAIVHATSTLIQKRHLV-KFVCITMWFLSLVLSLPIFILRT 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TVNLYSSYLILAFISLDRYLAIVHAINSQRPRKLLAEKVVYVGVWIPALLLTIPDEIFAN 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SLVMLVILYNRSTCSVTDVYLLNLAIADLFFALTLPVWAASKVNGWIFGSFLCKVFSFLQ 125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNYT-EEMGSGDYDSMK------EPCFREENANFNKIFLPTIYSIIFLTGIVGN 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ILGILHSCLNPLIYAFIGQKFR----HGL--
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Pred. No. 2
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Mismatches
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C;Accession: JQ1231; A40465
C;Accession: JQ1231; A40465
C;Accession: JQ1231; Munger, W.E.; Kozlosky, C.; VandenBos, T.; Fill.
Biochem. Biophys. Res. Commun. 179, 784-789, 1991
A;Title: Molecular characterization of the interleukin-8 receptor number: JQ1231; MUID:91378994
                                                                                                                                                                                                                                 A; Molecule type: mRNA
A; Residues: 1-355 < LEED
A; Cross-references: GB.M82873; NID:g165440;
                                                                                                                                                                                                                                                                                                                                    A;Cross-references: GB.M74240; NID:g165438; PID:g165439
R;Lee, J.; Kuang, W.J.; Rice, G.C.; Wood, W.I.
J. Immunol. 148, 1261-1264, 1992
A;Title: Characterization of complementary DNA clones encoding A;Reference number: A46483; MUID:92148149
A;Accession: A46483
                                                                                                                                                             A; Experimental source: neutrophils
A; Note: sequence extracted from NCBI backbone (NCBIN:81526, NCBIP:81530)
C; Keywords: G protein-coupled receptor; transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             interleukin-8 receptor - rabbit
C;Species: oryctolagus cuniculus (domestic rabbit)
C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992
C;Accession: JQ1231; A46483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: DNA
A; Residues: 1-355 <BEC>
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A; Cross-references: EMBJ
A; Experimental source: 1
C; Genetics:
                                                          Matches
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MEGISIYTSDNYTEEMGSGDYDSMKEPCFREENANFNKIFLPTIYSIIFLTGIVGNGLVI 60
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                                                 Score 564; DB
Pred. No. 3.6e
71; Mismatches
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Pred. No. 3.3
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MTDLWTWFEDEFANATGMPPVEKDYSPCL-VVTQTLNKYVVVVIYALVFLLSLLGNSLVM

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RESULT 10
A55735
G protein-coupled receptor EBI1 - mouse
C;Species: Mus musculus (house mouse)
C;Date: 07-Jul-1995 #sequence_revision 07-Jul-1
C;Accession: A55735
R;Schweickart, V.L.; Raport, C.J.; Godiska, R.;
Genomics 23, 643-650, 1994
A;Title: Cloning of human and mouse EBI1, a lym
A;Reference number: A55735; MUID:95154835
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-378 <SCH>
A;Cross references: GB:L31580; NID:9468340; PII
C;Keywords: G protein-coupled receptor
RESULT 11
A39445
interleukin-8 receptor type A - h
N;Alternate names: interleukin-8
C:Species: Homo sapiens (man)
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;Species: Mus musculus (house mouse)
;Date: 07-Jul-1995 #sequence_revision 07-Jul-1995 #text_change 17-Mar-1999
;Accession: A55735
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                                                                                                                                                                              LGAKFKTSAQHALTSVSRGSS--LKILSKGKRGGHSSVSTESESSSFHS 351
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                                                                                                                                        IGVKFRSDLFKLFKDLGCLSQERLRHWSSCRHVRNASVSMEAETTTTFS
                                                                                                                                                                                                                      VVVFIVFQLPYNGVVLAQTVANFNITNSSCETSKQLNIAYDVTYSLASVRCCVNPFLYAF
                                                                                                                                                                                                                                                          ILAFFACWLPYYIGISIDSFILLEIIKQGCEFENTVHKWISITEALAFFHCCLNPILYAF
                                                                                                                                                                                                                                                                                                  RCSLVSAQVEALITIQVAQMVFGFLVPMLAMSFCYLIIIRTLLQARNFERNKAIKVIIAV
                                                                                                                                                                                                                                                                                                                                          ICDRFYPNDLWVVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKALKTTVIL
                                                                                                                                                                                                                                                                                                                                                                                CISIDRYVAIVQAVSRHRHRARVLLISKLSCVGIWMLALFLSIPELLYSGLQKNSGEDTL 208
                                                                                                                                                                                                                                                                                                                                                                                                                      FISLDRYLAIVHAT -- NSQRPRKLLAEKVVYVGVWIPALLLTIPDFIFANV -- SEADDRY 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                              LKTMTDTYLLNLAVADILFLLILPFWAYSEAKSWIFGVYLCKGIFGIYKLSFFSGMLLLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LRSMTDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNLYSSVLILA 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TDDYIGENTTVDYTLYESVCFKKDVRNFKAWFLPLMYSVICFVGLLGNGLVILTYIYFKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SDNYTEEMGSGDYDSMKEPCFREENANFNKIFLPTIYSIIFLTGIVGNGLVILVMGYQKK 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NPILYAFLGAKFKTSAQHALTSVSRG-SSLKILSKGKRGGHSSVSTESESS 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MRVIFAVVLIFLLCWLPYNLVLLADTLMRTHVIQETCQRRNDIDRALDATEILGFLHSCL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LVMGYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNL
||:|:|:|||||:|::|||||:::|||
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NNSSPVCYEDLGHNTAKWRMVLRILPHTFGFILPLLVMLFCYGFTLRTLFQAHMGQKHRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRYIC -- DRFYPNDLWVVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YSSVLILAFISLDRYLAIVHATNSQRPRKLLAEKVVYVGVWIPALLLTIPDFIFANV-SE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LVILYSRSNRSVTDVYLLNLAMADLLFALTMPIWAVSKEKGWIFGTPLCKVVSLVKEVNF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YSGILLLACISVDRYLAIVHATRTLTQKRHLV-KFICLGIWALSLILSLPFFLFRQVFSP 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30.8%;
                     receptor,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 563; DB 2; 1
Pred. No. 4.6e-39;
7; Mismatches 147;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PID:g468341
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 378
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                                                                                                                                        377
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RESULT
A53752
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A;Cross-references: GDB:135039; OMIM:146929
A;Map position: 2q35-2q35
C;Keywords: G protein-coupled receptor; glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A:Cross-references: EMBL:U11871; NID:g511806; R:Holmes, W.B.; Lee, J.; Kuang, W.J.; Rice, G. Science 253, 1278-1280, 1991
A:Title: Structure and functional expression ca:Reference number: A39445; MUID:91368199
A:Accession: A39445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A:Molecule type: DNA
A:Residues: 1-350 <RES>
A:Residues: 1-350 <RES>
A:Cross references: EMBL:X65858; NID:g312046; PID:g312047
A:Cross references: EMBL:X65858; NID:g312046; PID:g312047
A:Ahuja, S.K.; Shetty, A.; Tiffany, H.L.; Murphy, P.M.
J. Biol. Chem. 269, 26381-26389, 1994
A:Title: Comparison of the genomic organization and promot A:Reference number: I37898; MUID:95014476
A:Accession: I38710
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Date: 22-Jan-1993 #sequence_revision 12-Apr-1996 #text_change 24-Sep-1998 C;Accession: I37449; I38710; I38711; A39445 R;Mollereau, C; Muscattelli, F; Mattei, M.G.; Vassart, G.; Parmentier, M. Genomics 16, 248-251, 1993 Interleukin 8 receptor gene (IL8RA) maps to the A;Title: The high-affinity interleukin 8 receptor gene (IL8RA) maps to the A;Accession: I37449; MUID:93252387
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A;Residues: 1-275,'T',277-350 <HOL>
A;Cross-references: GB:M68932; NID:g186369;
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A; Residues: 1-350 < RE2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: mRNA
A; Residues: 1-16 <RE3>
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                                                                                           311 NFRHGFLKILAMHGLVS
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                                                                                                                                                                                                                                                                                                                          YPNDL--WVVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKALKTTVILILA 247
                                                                                                                                     KF----KTSAQHALTS
                                                                                                                                                                                  FLICWLPYNLVLLADTLMRTQVIQESCERRNNIGRALDATEILGFLHSCLNPIIYAFIGQ
                                                                                                                                                                                                                                                                           LGNDTAKWRMVLRILPHTEGEIVPLEVMLECYGETLRTLEKAHMGQKHRAMRVIFAVVLI
                                                                                                                                                                                                                                                                                                                                                                                                                     SLDRYLAIVHATNSQRPRKLLAEKVVYVGVWIPALLLTIPDFIFANVSEADDRY-ICDRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SMTDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNLYSSVLILAFI 130
                                                                                                                                                                                                                              FFACWLPYYIGISIDSFILLEIIKQGCEFENTVHKWISITEALAFFHCCLNPILYAFLGA
                                                                                                                                                                                                                                                                                                                                                                         SVDRYLAIVHATRTLTOKRHLV-KFVCLGCWGLSMNLSLPFFLFRQAYHPNNSSPVCYEV 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SVTDVYLLNLALADLLFALTLPIWAASKVNGWIFGTFLCKVVSLLKEVNFYSGILLLACI 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NFT----GMPPADEDYSPCML-ETETLNKYVVIIAYALVFLLSLLGNSLVMLVILYSRVGR 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity 38.:
21; Conservative
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                                                                                                                                     319
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 559.5; DB 2;
Pred. No. 8.2e-39;
6; Mismatches 127;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PID:g186370
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               membrane
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interleukin-8 receptor (clone 5Bla) - rabbit (5 Species: Oryctolagus cuniculus (domestic rabbit) C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 C;Accession: A53752 R;Prado, G.N.; Thomas, K.M.; Suzuki, H.; LaRosa, G.

G.J.;

Wilkinson,

N.; Folco,

E)

#text_change

10-Sep-1997

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A;Molecule type: mRNA
A;Residues: 1-358 <PRA>
A;Cross-references: GB:L244445; NID:9437661; PID:9437662
C;Keywords: G protein-coupled receptor; transmembrane pu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          J. Biol. Chem. 269, 12391-12394, 1994
A;Title: Molecular characterization of a novel rabbit interleukin-8 receptor isotype.
A;Reference number: A53752; MUID:94230294
A;Accession: A53752
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                                                                                                                                                                                                                                                                                                                                                                                                              lymphocyte-specific G-protein-coupled receptor N; Alternate names: Burkitt's lymphoma receptor C; Species: Homo sapiens (man) C; Date: 07-Jul-1995 #sequence_revision 07-Jul-1 C; Accession: B55735; S52443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Qy
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                                                                                                                                                                                                      A;Cross-references: GB:L31581; NID:9468319; PID:9468320 R;Burgstahler, R.; Kempkes, B.; Staeube, K.; Lipp, M. submitted to the EMBL Data Library, February 1995
                                                                                                                                                                                                                                                                A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-378 <SCH>
                                                                                                                                                                                                                                                                                                                                    R;Schweickart, V.L.; Raport, C.J.; Godiska, Genomics 23, 643-650, 1994
A;Title: Cloning of human and mouse EBI1, a A;Reference number: A55735; MUID:95154835
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    δÃ
A;Gene: GDB:CMKBR7; EBI1; BLR2;
A;Cross-references: GDB:342065;
A;Map position: 17q12-17q21.2
                                                                                                                                                 A; Reference number: S52443
A; Accession: S52443
                                                                         A; Cross-references: EMBL: X84702
                                                                                             A; Molecule type: DNA
A; Residues: 21-378 <
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Best Local
                                                                                                                                                                                      Description: The expression of the chemokine
                                                                                                                                                                                                                                                                                                                     Accession: B55735
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                                                                                                                                Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FLHSCLNPIIYAFIGQKFRYGLLKILAAHGLI----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FFHCCLNPILYAFLGAKF-----KTSAQHALTSVSRGSSLKILSKGKRGGHSSVSTESES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RNAIFPPNSSPVCYEDMGNSTAKWRMVLRILPQTFGFILPLLVMLFCYVFTLRTLFQAHM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GNSLYMLVILYSRSTCSVTDVYLLNLAIADLLFATTLPIWAASKVHGWTFGTPLCKVVSL 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FTWENYSYEDFFGDFSNYSYSTDLPPTLLDSAPC-RSESLETNSYVVLITYILVFLLSLL 62
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                                                                                               <BUR>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               66;
                         OMIM: 600242
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Pred.
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No. 1.
                                                                                                                                                                                                                                                                                                                                                                                                  R.; Byers,
                                                                                                                                                                                                                                                                                                                                                             lymphoid-specific
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    r EBI1 - human
2; Epstein-Ra
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               --SKEFLAKESR--PSFVASSSGN
                                                                                                                                                                                          receptor BLR2/EBI1 is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Epstein-Barr virus induced
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                                                                                                                                                                                                                                                                                                                                                                                                  Eddy Jr.,
                                                                                                                                                                                                                                                                                                                                                               G-protein-coupled
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                    R.L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 353
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C; Keywords: G protein-coupled receptor

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R;Raport, C.J.; Schweich
Gene 163, 295-299, 1995
A;Title: The orphan G-pu
A;Reference number: JC4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Species: Homo sapiens (man)
C;Date: 16-Nov-1995 #sequence_revision 08-Feb-1996
C;Accession: JC4304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      δÃ.
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                                                                                                                                                                                                                                                                                                         A; Map position: 3pter-p21
C; Keywords: G protein-coupled receptor; lymphokine; transmembrane
F; 35-57/Domain: transmembrane #status predicted <TMI>
F; 66-88/Domain: transmembrane #status predicted <TM2>
                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: GB:U20350; NID:g665580; PID:g665581
A;Experimental source: peripheral blood mononuclear cell
C;Comment: This protein is a cell-surface receptor which
C;Comment: This protein is a key regulator of many immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      밁
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                                                                                                                                                                                                         F;104-125/Domain: transmembrane *status predicted <TM3>F;146-165/Domain: transmembrane *status predicted <TM4>F;146-165/Domain: transmembrane *status predicted <TM5>F;197-217/Domain: transmembrane *status predicted <TM5>F;230-254/Domain: transmembrane *status predicted <TM6>F;275-296/Domain: transmembrane *status predicted <TM7>
                                                                                                                                                                                                                                                                                                                                                                                                                       C;Comment: This protein is a cell C;Comment: This protein is a key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          orphan G-protein-coupled receptor N; Alternate names: V28 protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: mRNA
A; Residues: 1-355 < RAP>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Accession: JC4304
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Best Local S
Matches 116
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                                                                                                                 Matches
                                                                                                                                                     Query Match
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hes 116; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CISIDRYVAIVQAVSAHRHRARVLLISKLSCVGIWILATVLSIPELLYSDLQRSSSEQAM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TDDYIGDNTTVDYTLFESLCSKKDVRNFKAWFLPIMYSIICFVGLLGNGLVVLTYIYFKR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ICDRFYPNDLWVVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKALKTTVIL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ILAFFACWLPYYIGISIDSFILLEIIKQGCEFENTVHKWISITEALAFFHCCLNPILYAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RCSLITEHVEAFITIQVAQMVIGFLVPLLAMSFCYLVIIRTLLQARNFERNKAIKVIIAV
LRSMTDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNLYSSVLILA
                                   DNYTEEMGSG-DYDSMKEPCFREENANFNKIFLPTIYSIIFLTGIVGNGLVILVMGYQKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IGVKFRNDLFKLFKDLGCLSQEQLRQWSSCRHIRRSSMSVEAETTTTFS
                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Schweickart, V.L.; Eddy Jr.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            G-protein-coupled receptor-encoding JC4304; MUID:96011651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30.4%;
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                                                                                                                   68;
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Pred. No. 1.4e-38;
9; Mismatches 148
                                                                                                                 Score 549.5; DB 2;
Pred. No. 5.5e-38;
8; Mismatches 144;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R.L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         148;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Shows,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gray, P.W.
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MDCRI5 protein - human
(C:Species: Homo sapiens (man)
C:Species: Homo sapiens (man)
C:Accession: S56162
R:Barella, L.; Loetscher, M.; Tobler, A.; Baggiolini, M.; Moser, B.
Biochem. J. 309, 773-779, 1995
A:Reference variation of a novel heptahelical leucocyte receptor through alternati
A:Reference number: S56162
A:Accession: 
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                                                                                                                                                                                                                                                                                                                          234
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62 AVAEGSVGWVLGTFLCKTVIALHKVNFYCSSLLLACIAVDRYLAIVHAVHAYRHRRLLSI 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            94 WAVDAVANWYFGNFLCKAVHVIYTVNLYSSVLILAFISLDRYLAIVHATNSQRPRKLLAE 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              34
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                                                                                                                                                                                                                                              SVSRGSSLKILSKGKRGGHSSVSTESESSS 348
                                                                                                                                                                                                                                                                                                                      HITCGTIWLVGFLLALPEILFAKVSQG------HHNNSLPRCTFSQENQAETHAWFTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ANENKIFLPTIYSIIFLTGIVGNGLVILVMGYQKKLRSMTDKYRLHLSVADLLFVITLPF 93
                                                                                                                                                                      KLGCTSPASLCQLFPSWRRSSLS-ESENAT 322
                                                                                                                                                                                                                                                                                                                                                                               ISIDSFILLEIIKQGCEFENTVHKWISITEALAFFHCCLNPILYAFLGAKFKTSAQHALT
                                                                                                                                                                                                                                                                                                                                                                                                                                                          RFLYHVAGFLLPMLVMGWCYVGVVHRLRQAQRRPQRQKAVRVAILVTSIFFLCWSPYHIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ASFKAVFVPVAYSLIFLLGVIGNVLVLVILERHROTRSSTETFLFHLAVADLLLVFILPF 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GEKFRRYLYHLY-----GKCLAVLCGRSVHVDFSSSESQRSRHGSVL--SSNFTYHTS 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DYPEVLQEIWPVLRNVETNFLGFLLPLLIMSYCYFRIIQTLFSCKNHKKAKAIKLILLVV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                453288 seqs, 56848278 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BLOSUM62
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1830
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pending_Patents_AA: *
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   September 14, 1999, 09:51:02;
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11:
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: /cgn2_6/ptodata/2/paa/US084B_COMB.pep:*
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: /cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep:*
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /cgn2_6/ptodata/2/paa/PCTUS9_COMB.pep:*
/cgn2_6/ptodata/2/paa/US07_COMB.pep:*
/cgn2_6/ptodata/2/paa/US080_COMB.pep:*
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2_6/ptodata/2/paa/US083_COMB.pep:*
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(without alignments)
864.389 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	% Query Match Length	₽B	ID	Description
1	1830	100.0	352	- }	PCT-US93-10672-2	Sequence 2, Appli
2	1830	100.0	352	σ	US-08-308-880-2	Sequence 2, Appli
ω	1830	100.0	352	7	US-08-441-562-2	ν.
4	1830	100.0	352	12	US-08-801-228-4	4
5	1830	100.0	352	12	US-08-801-238-4	4.
σ	1830	100.0	352	12	US-08-802-627-4	4
7	1830	100.0	352	12	US-08-802-627A-4	4
80	1830	100.0	352	15	US-09-104-063-4	Sequence 4, Appli
9	1830	100.0	352	15	US-09-104-296-4	4
10	1808		356	15	US-09-122-068-2	ν,
11	1789		352	4	US-08-182-962-6	`
12	1789		352	7	US-08-446-669-6	
13	1789	97.8	352	7	US-08-450-393-6	σ,
14	1752		337	2	US-07-977-452A-21	21,
15	1752		337	ъ	US-08-245-242-46	46,
16	1752	95.7	337	22	US-09-299-843A-46	Sequence 46, Appl
17	600.5	32.8	360	10	US-08-675-814-14	14,
18	600.5	32.8	360	12	US-08-875-573-20	Sequence 20, Appl
19	600.5	32.8	360	12	US-08-887-977-16	16.
20	600.5	32.8	360	13	US-08-989-107-34	34,
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4	4	4	4	4	4	ω	38	ω	ω	w	w	ω	ω	ω	w	2	2	2	2	2	2	N	2	
5 557.5	4 557.5			1 567.5																5 594	4 600.5		2 600.5	
							31.0													32.5		32.8		
350	350	378	378	415	415	360	1065	355	355	355	355	355	355	353	353	355	368	368	360	123	360	360	360	
1	ب	22	G	۳	μ	16	10	7	7	7	σ	σ	4	↦	ب	μ	12	11	12	ဖ	16	14	14	
PCT-US99-11842-27	PCT-US93-10672-3	US-09-299-843A-66	US-08-245-242-66	PCT-US96-00499A-2	PCT-US96-00499-2	US-09-236-166-4	US-08-605-185-22	US-08-450-393-8	US-08-446-669-8	US-08-441-562-4	US-08-390-000A-5	US-08-308-880-4	US-08-182-962-8	PCT-US96-00499A-9	PCT-US96-00499-9	PCT-US93-10672-4	US-08-829-839-2	US-08-709-838-2	US-08-833-752-10	US-08-513-974B-330	US-09-232-878-2	US-09-067-447-34	US-09-067-447-34	
Sequence 27, Appl	Sequence 3, Appli	Sequence 66, Appl	Sequence 66, Appl	Sequence 2, Appli	Sequence 2, Appli	Sequence 4, Appli	Sequence 22, Appl	Sequence 8, Appli	Secuence 8, Appli	Sequence 4, Appli	Seguence 5, Appli	4,		Sequence 9, Appli	Sequence 9, Appli	Sequence 4, Appli	Sequence 2, Appli	Sequence 2, Appli	Sequence 10, Appl	Sequence 330, App	Sequence 2, Appli	Sequence 34, Appl	Sequence 34, Appl	

ALIGNMENTS

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PCT-US93-10672-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 1
PCT-US93-10672-2
                                                                                                    FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Fitts, Renee A.

REGISTRATION NUMBER: 35,136

REFERENCE/DOCKET NUMBER: 806

TELECOMMUNICATION: INFORMATION:

TELEPHONE: 415/225-1489

TELEPAX: 415/952-9881

TELEEX: 910/371-7168

INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2, Application PC/TUS9310672
GENERAL INFORMATION:
APPLICANT: GENENTECH, INC.
TITLE OF INVENTION: CC-CHEMOKINE RECEPTOR
NUMBER OF SEQUENCES: 11
                                        SEQUENCE CHARACTERISTICS:
LENGTH: 352 amino acid
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patin (Genentech)
CURRENT APPLICATION NUMBER: PCT/US93/10672
FILING DATE:
FILING DATE:
                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: U:
ZIP: 94080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
                    TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE:
                                        : 352 amino acids amino acid
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                                                                             US-08-308-880-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2, Application US/08308880 GENERAL INFORMATION:
 Query Match
Best Local Similarity
Matches 352; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best
                                                                                                                                                 TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1489
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                        CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/9;
FILING DATE: 10-NOV-1992
                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM: MEDIUM TYPE: 5.25 inch,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: RICHARD HORUK, KULDEEP NEOTE, THOMAS SCHALL TITLE OF INVENTION: CC-CHEMOKINE RECEPTOR
                                                                                                                                     SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                           FILING DATE: 10-NOV-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61
                                                                                                          TYPE: amino acids
                                                                                                                                                                                                                               NAME: Fitts, Renee A.
REGISTRATION NUMBER: 35
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET:
                                                                                             TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MEGISIYTSDNYTEEMGSGDYDSMKEPCFREENANFNKIFLPTIYSIIFLTGIVGNGLVI 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LYAFLGAKFKISAQHALISVSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 352
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LVMGYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TVILILAFFACWLPYYIGISIDSFILLEIIKQGCEFENTVHKWISITEALAFFHCCLNPI 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DDRYICDREYPNDLWVVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKALKT 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LVMGYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DDRYICDRFYPNDLWVVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKALKT 240
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, Mismatches
Score 1830; DB 6; Pred. No. 2.1e-167; Mismatches 0;
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                              Length 352;
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US-08-441-562-2
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 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121
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                                                                            TYPE: Amino Acid
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                                                                                        LENGTH:
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Sequence 2, Application US/08441562 GENERAL INFORMATION:
             TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                       FILING DATE: 19-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/974
FILING DATE: 10-NOV-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/30
FILING DATE: 19-SEP-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM: MEDIUM TYPE: 3.5 inch,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech,
STREET: 460 Point San
                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA: APPLICATION NUMBER: US
                                                                                                    REFERENCE/DOCKET NUMBER: POTELECOMMUNICATION INFORMATION: 415/225-5530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 YSSVLILAFISLDRYLAIVHATNSQRPRKLLAEKVVYVGVWIPALLLTIPDFIFANVSEA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WinPatin (Genentech)
                                                                                                                                                                    NAME: LOVE, Richard B
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEGISIYTSDNYTEEMGSGDYDSMKEPCFREENANFNKIFLPTIYSIIFLTGIVGNGLVI
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352 amino acids
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                                                                                                                                                                         34,659
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Sequence 4, Application US/08801228 GENERAL INFORMATION:
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                          INFORMATION FOR SEQ ID NO: 4: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 94080

COMPUTER READABLE FORM;
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Lee, James
APPLICANT: Wood, William I.
TITLE OF INVENTION: METHODS FOR DETECTION AND AMPLIFICATION
TITLE OF INVENTION: PF4A RECEPTOR NUCLEIC ACID
                                                                                                            NAME: LOVE, RICHARD B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: PO
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-5530
                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/801,228
FILING DATE: 19-Feb-1997
CLASSIFICATION: 45
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/284586
FILING DATE: 10-AUG-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech
                                                                                                                                                                                                               APPLICATION NUMBER: 07/810782 FILING DATE: 19-DEC-1991 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/0
FILING DATE: 11-JUN-1993
PRIOR APPLICATION DATA:
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                                                                  TELEPHONE: 415/225-55
TELEFAX: 415/952-9881
TELEX: 910/371-7168
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             amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 352; Conserv
APPLICATION NUMBER: 08/076093
FILING DATE: 11-JUN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/810782
FILING DATE: 19-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: LOVE, Richard B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: P0706P2P1D1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-5530
                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/801,238
FILING DATE: 19-Feb-1997
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/284586
FILING DATE: 10-AUG-1994
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM: MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Lee, James
APPLICANT: Wood, William
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Genentech
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CITY: South San Francisco
STATE: California
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    94080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E: Genentech, Inc.
460 Point San Bruno Blvd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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US-08-801-228-4

COUNTRY:

USA

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; TOPOLOGY: US-08-801-238-4
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Best Local
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INFORMATION FOR SEO ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 352 amino acids
TYPE: Amino Acid
               FILING DATE: 10-AUG-1994
PRIOR APPLICATION DATA:
RAPPLICATION UNMBER: 08/076
FILING DATE: 11-JUN-1993
PRIOR APPLICATION UNMBER: 07/810
FILING DATE: 19-DEC-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Lee, James
APPLICANT: Wood, William I.
TITLE OF INVENTION: NUCLEIC ACID ENCODING PF4A RECEPTOR
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                     PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                             SOFTWARE: WinPatin (Ge CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: 3.5 inc
 ATTORNEY/AGENT
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                                                                                                                                                                                                                                                                              MEDIUM TYPE: 3.5 inch, 1.44 Mb COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                          STREET: 460 Point San Brun
CITY: South San Francisco
STATE: California
COUNTRY: USA
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                                                                                                                                                  APPLICATION NUMBER: 08/284586
                                                                                                                                                                                         CLASSIFICATION:
                                                                                                                                                                                                        APPLICATION NUMBER: US/0 FILING DATE: 19-Feb-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MEGISIYTSDNYTEEMGSGDYDSMKEPCFREENANFNKIFLPTIYSIIFLTGIVGNGLVI
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Pred. No. 2.1e-167;
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MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
COCUMENTS: Windelin (Generical)
                                                  CLASSIFICATION: 514
PRIOR APPLICATION DATA:
08/284586
                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: NUCLEIC ACID ENCODING PF4A RECEPTOR NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                   PRIOR APPLICATION DATA:
                                                                                                                                                    SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Lee, James
APPLICANT: Wood, William I.
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CITY: South San Francisco
STATE: California
                                   APPLICATION NUMBER: 08/2 FILING DATE: 10-AUG-1994
                                                                                                               APPLICATION NUMBER: US/0 FILING DATE: 19-Feb-1997
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APPLICATION NUMBER:
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USA

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US-08-802-627-4
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TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 352 amino acids
TYPE: Amino Acid
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Best Local Similarity
Matches 352; Conserv
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TELEPHONE: 415/225-5530
TELEPHONE: 415/25-9881
                           301 LYAFLGAKFKTSAQHALTSVSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 352
                                                                                                                                        241 TYILILAFFACWLPYYIGISIDSFILLEIIKQGCEFENTYHKWISITEALAFFHCCLNPI 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: Linear
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LYAFLGAKFKTSAQHALTSVSRGSSLKILSKGKRGGHSSVSTESESSSFHSS
                                                                                                            TVILILAFFACWLPYYIGISIDSFILLEIIKQGCEFENTVHKWISITEALAFFHCCLNPI
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US-09-104-063-4
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Best Local s
Matches 352
                                                                                                                                                                                                                                                              Sequence 4, Application US/09104063
GENERAL INFORMATION:
APPLICANT: Lee, James
APPLICANT: Wood, WILLIAM I.
TITLE OF INVENTION: PF4A Receptors
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
          COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb flopp

MEDIUM TYPE: 3.5 inch, 1.44 Mb flopp

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WilPatin (Genentech)

CURRENT APPLICATION DATA:

**POTICATION NUMBER: US/09/104,063
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Love, Richard B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: P070
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-5530
TELEFAX: 415/952-9881
TELEFX: 910/371-7168
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SEQUENCE CHARACTERISTICS:
LENGTH: 352 amino acids
TYPE: Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 11-JUN-1993
PRIOR APPLICATION DATA:
APPLICATION UNMBER: 07/8:
FILING DATE: 19-DEC-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 301 LYAFLGAKFKTSAQHALTSVSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 352
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                                                                                                                                                                                          STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
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APPLICATION NUMBER: FILING DATE: 24-Jur
                                                                                                                                                         COUNTRY: U
                                                                                                                                                                                                                                                  ADDRESSEE:
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  24-June-1998
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                                                                                                               1.44 Mb floppy disk
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                                                                                                                               Sequence 4, Application US/09104296
GENERAL INFORMATION:
APPLICANT: Lee, James
APPLICANT: Wood, WILLIAM I.
TITLE OF INVENTION: PF4A Receptors
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEO ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 352 amino acids
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Matches
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TELEPHONE: 415/952-9881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 19-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B.
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATA:
PRIOR APPLICATION DATA:
08/076093
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APPLICATION NUMBER: 08/664228
FILING DATE: 06-JUN-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 11-JUN-1993
PRIOR APPLICATION DATA:
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APPLICATION NUMBER: 08/701265
FILING DATE: 22-AUG-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   241 TVILILAFFACWLPYYIGISIDSFILLEIIKQGCEFENTVHKWISITEALAFFHCCLNPI 300
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                                               STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
                  COUNTRY: UZIP: 94080
                                                                                        ADDRESSEE: Genentech, STREET: 1 DNA Way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 LVMGYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNL 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Love, Richard REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER:
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RESULT 10
US-09-122-068-2
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Sequence 2, Application US/09122068
GENERAL INFORMATION:
GENERAL PILLARISETTI, KODANDARAM
APPLICANT: GUPTA, SHALLEY
TITLE OF INVENTION: CXCR4B: A HUMAN
TITLE OF INVENTION: OF CXCR4 CHEMOK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches 352;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: LOVE, RICHALL 34,659
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: P070
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 352 amino acid
TYPE: Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: 07/810782 FILING DATE: 19-DEC-1991 ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER: 08/70
FILING DATE: 22-AUG-1996
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CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: 08/664228 FILING DATE: 06-JUN-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/09/104,296 FILING DATE: 24-June-1998
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SOFTWARE: WinPati
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COMPUTER: IE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 1830; DB 15; 100.0%; Pred. No. 2.1e-167; vative 0; Mismatches 0;
   CXCR4B: A HUMAN SPLICE VARIANT OF CXCR4 CHEMOKINE RECEPTOR
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; TOPOLOGY: line
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TELEX: 846169
INFORMATION FOR SEQ ID NO: 7
SEQUENCE CHARACTERISTICS:
LENGTH: 356 amino acids
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Best Local Similarity
Matches 347; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Prestia, Paul FF
REGISTRATION NUMBER: 23,031
REFERENCE/DOCKET NUMBER: GH
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-07-0700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: FastSEQ for Windows Version CURRENT APPLICATION DATA:
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ATTORNEY/AGENT INFORMATION:
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308 FLGAKFKTSAQHALTSVSRGSSLKILSKGKRGGHSSVSTESESSSFHSS
                      304 FLGAKFKTSAQHALTSVSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 352
                                                                                      244 LILAFFACWLPYYIGISIDSFILLEIIKQGCEFENTVHKWISITEALAFFHCCLNPILYA
                                                                                                                                188 YICDRFYPNDLWVVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKALKTTVI
                                                                                                                                                   184 YICDREYPNDLWVVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKALKTTVI
                                                                                                                                                                                                                    124 VLILAEISLDRYLAIVHATNSQRPRKLLAEKVVYVGVWIPALLLTIPDFIFANVSEADDR 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                    64 GYQKKLRSMTDKYRLHLSVADLLEVITLPEWAVDAVANWYFGNFLCKAVHVIYTVNLYSS 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Ratner of STREET: P.O. Box 98 CITY: Valley Forge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM:
SOFTWARE: FastSEC
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                                                                                                                                                                                                                                                                                                                                                      4 ISIYTSDNYTEEMGSGDYDSMKEPCFREENANFNKIFLPTIYSIIFLTGIVGNGLVILVM 63
                                                                COTYTSDNYTEEMGSGDYDSMKEPCFREENANFUKIFLPTTYSTIFLTGTVGNGLVILVM
                                                                                                                                                                                                  VLILAFISLDRYLAIVHATNSQRPRKLLAEKVVYVGVWIPALLLTIPDFIFANVSEADDR
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O. Box 980
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                                                                                                                                                                                                                                                                                                                                                                                                   Score 1808; DB 15;
Pred. No. 2.7e-165;
1; Mismatches 1;
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RESULT 11
US-08-182-962-6
; Sequence 6, Application US/08182962
; GENERAL INFORMATION:
; APPLICANT: Charo, Israel Coughlin, Shaun

303

307

247

243 187

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RESULT 12
US-08-446-669-6
; Sequence 6, Application US/08446669
; GENERAL INFORMATION:
; APPLICANT: Charo, Israel
; APPLICANT: COughlin, Shaun
; TITLE OF INVENTION: MAMMALIAN MC
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Best Local Similarity
Matches 346; Conserv
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TELEX: 380816CooleyPA
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Cserr, Luann
REGISTRATION NUMBER: 31,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
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HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-494-7622
TELEFAX: 415-857-0663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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                                                                                                                                                                           301 LYAFLGAKFKTSAQHALTSVSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 352
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STATE: Californ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER:
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5 Palo Alto Square
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98.3%;
MAMMALIAN MONOCYTE CHEMOATTRACTANT
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Pred. No. 1.8e-163;
0; Mismatches 6; Indels
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Sequence 6, Application US/08450393;
GENERAL INFORMATION:
APPLICANT: Charo, Israel
APPLICANT: Coughlin, Shaun
TITLE OF INVENTION: PROTEIN REC:
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Best Local Sim
Matches 346;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Neeley, Richard
REGISTRATION NUMBER: 30,092
REFERENCE/DOCKET NUMBER: UCAI
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-843-5000
TELEFAX: 415-857-0663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: J. STREET: DIO Alto CITY: Palo Alto CTATE: California
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FILING DATE: May 25, 1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Neeley, Richard
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HYPOTHETICAL:
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LENGTH: 352 amino acid
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
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NUMBER OF SEQUENCES:
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98.3%;
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   MAMMALIAN MONOCYTE CHEMOATTRACTANT PROTEIN RECEPTORS
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Pred. No. 1.8e-163;
0; Mismatches 6;
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NUMBER OF SEQUENCES: CORRESPONDENCE ADDRE

ADDRESS:

Godward Castro Huddleson & Tatum

ADDRESSEE: COULEY CONTREET: 5 Palo Alto Square

CORRESPONDENCE ADDRESS:

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; HYPOTHETICAL: US-08-450-393-6
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US-07-977-452A-21
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Best Local :
                                                                     Sequence 21, Application US/07977452A GENERAL INFORMATION:
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NAME: CSETT, LUANN
REGISTRATION UNMER: 31,822
REFERENCE/DOCKET NUMBER: UCAL
TELECOMMUNICATION: INFORMATION:
TELEPHONE: 415-843-5165
TELEFAX: 415-8857-0663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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CITY: Palo Alto
STATE: California
COUNTRY: USA
            APPLICANT: Godiska, Ronald APPLICANT: Gray, Patrick W. APPLICANT: Schweikart, Vicki L. TITLE OF INVENTION: Novel Seven
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98.3%;
              Novel Seven
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Pred. No. 1.8e-163;
0; Mismatches 6;
                 Transmembrane Receptors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 352;
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                                                                                                                                                     RESULT 15
US-08-245-242-46
Sequence 46, Application US/08245242
GENERAL INFORMATION:
APPLICANT: Godiska, Ronald
APPLICANT: Schweikart, Vicki L.
TITLE OF INVENTION: Novel Seven Transmembrane Receptors
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 30:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 346-5750
THE TENEY. (312) 346-5750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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LENGTH: 337 amino acids
TYPE: amino acid
TOPOLOGY: linear
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ADDRESSEE: Bicknell
STREET: Two First National Pla
CITY: Chicago
STATE: Illinois
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16 MGSGDYDSMKEPCFREENANFNKIFLPTIYSIIFLTGIVGNGLVILVMGYQKKLRSMTDK 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MGSGDYDSMKEPCFREENANFNKIFLPTIYSIIFLTGIVGNGLVILVMGYQKKLRSMTDK 60
                                                                                                                                                                                                                                                                                                                                                                                VVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKALKTTVILILAFFACWLPY
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                                                                                                                                                                                                                                                                                                                                                                                                     VVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKALKTTVILILAFFACWLPY 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                        LAIVHATNSQRPRKLLAEKVVYVGVWIPALLLTIPDFIFANVSEADDRYICDRFYPNDLW 180
                                                                                                                                                                                                                                 ALTSVSRGSSLKILSKGKRGGHSSVSTESESSSFHSS
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ilarity 100.0%;
Conservative 0
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Marshall, O'Toole, Gerstein, Murray &

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INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
ENROTH: 337 amino acids
TYPE: amino acid
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-245-242-46
Search completed: September 14, 1999, 09:52:21 Job time: 79 sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION UNMBER: US/08/245,242
FILING DATE:
CLASSIFICATION 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/153,848
FILING DATE: 17-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 07/977,452
FILING DATE: 17-NOV-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Noland, Greta E, REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31794
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6500
TELEFAX: (312) 474-0448
TELEX: 25-3856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 60606

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                    196 VVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKALKTTVILILAFFACWLPY 255
                                                                                                                                                                                                                                                                                                       ADDRESSEE: Mar:
ADDRESSEE: Bor:
STREET: 6300 Sc
CITY: Chicago
STATE: Illinois
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                                                                                                                                                           241 YIGISIDSFILLEIIKQGCEFENTVHKWISITEALAFFHCCLNPILYAFLGAKFKTSAQH 300
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Copyright (c) 1993 - 1998 Compugen
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/cgn2_6/ptodata/2/iaa/pcTUS9_cOMB.pep:*
/cgn2_6/ptodata/2/iaa/backfiles1.pep:*
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US-08-201-265-4
US-08-284-586-4
US-08-805-478-6
US-08-153-848-46
PCT-US95-00476-6
PCT-US95-00476-6
US-07-759-568-1
US-08-202-056-7
US-08-202-056-1
US-08-202-056-1
US-08-410-453A-1
US-08-410-454A-1
US-08-410-456A-1
US-08-410-456A-1
US-08-153-848-7
US-08-153-848-7
US-08-153-848-7
US-08-153-848-7
PCT-US93-11153-15
PCT-US93-11153-24
PCT-US93-11153-24
PCT-US93-11153-24
PCT-US93-11153-28
PCT-US93-11153-28
PCT-US93-11153-28
PCT-US93-11153-28
   US-08-202-056-5
US-08-076-093A-6
US-08-701-265-6
US-08-284-586-6
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APPLICATION NUMBER: US/08/202,056
FILING DATE: 25-FEB-1994
CLASSIFICATION: 436
PRIOR APPLICATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/677211
FILING DATE: 29-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: LOVE, RICHARD 34,659
REGISTRATION NUMBER: 706P3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-5530
TELECAS: 910/371-7168
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LEUCTH: 352 amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
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US-08-202-056-3
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US-08-202-056-3
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Patent No.
                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 352; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Genentech, Inc.

ADDRESSEE: Genentech, Inc.

STREET: 460 Point San Bruno Blvd

CITY: South San Francisco

STATE: California

COUNTRY: USA

ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 5.25 inch, 360 Kb floppy di

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: patin (Genentech)

CURRENT APPLICATION DATA:

ADDITICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Chuntharapai, P
APPLICANT: Hebert, Carolin
APPLICANT: Kim, Kyung Jin
APPLICANT: Lee, James
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION:
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                                                                        YSSVLILAFISLDRYLAIVHATNSQRPRKLLAEKVVYVGVWIPALLLTIPDFIFANVSEA

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US-08-383-750-2

US-08-383-751A-2

PCT-US93-09636-2

US-08-450-393A-2

PCT-US95-00476-2
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Pred. No. 6
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Matches
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Best Local Similarity
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                                                                                                                                                                                                                                                                                              TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb i
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/8
FILING DATE: 19-DEC-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: WinPatin (Gen
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Hebert, Caroline APPLICANT: Jin Kim, K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Lee, James
                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 29-MAR-
                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-5530
TELEFAX: 415/952-9881
                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 460 Point San Bruno Blvd CITY: South San Francisco STATE: California
                                                                                                                                                                                                                                 TYPE: Am:
TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                               REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
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 LVMGYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNL 120
                 LVMGYQKKLRSMTDKYRLHLSVADLLEVITLPEWAVDAVANWYFGNELCKAVHVIYTVNL 120
                                                                                                                                                                                                                                               Amino Acid
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                                                                                                                            100.0%; Score 1830; DB 1; ilarity 100.0%; Pred. No. 6.4e-144; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                 Linear
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                                                                                                                                                                                                                                                                                                                                                                                                              Richard B
                                                                                                                                                                                                                                                                                                                                                                                                                                                  29-MAR-1991
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US-08-701-265-4
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                                                                           ; TOPOLOGY: US-08-701-265-4
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GENERAL INFORMATION:
                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 352 amin
           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                   FILING DATE: 19-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION UNMBER: 07/677
FILING DATE: 29-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: LOVE, RICHARD B
REGISTRATION NUMBER: 34,65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech,
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APPLICANT: Hebert, Caroline
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                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 424
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION NUMBER: US/08/701,
APPLICATION NUMBER: US/08/701,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF
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                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 08/076093
FILING DATE: 11-Jun-1993
APPLICATION NUMBER: 07/810782
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 22-AUG-1996
                                                                                                                                                                                       TELEPHONE: 415/225-55
TELEFAX: 415/952-9881
                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YSSVLILAFISLDRYLAIVHATNSQRPRKLLAEKVVYVGVWIPALLLTIPDFIFANVSEA
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                 Score 1830; DB 2;
Pred. No. 6.4e-144;
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                                                NAME: Love, Richard B
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: 706P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-5530
TELEPHONE: 415/925-9881
TELEPX: 910/371-7168
INFORMATION FOR SEQ ID NO: 4:
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MEDIUM TYPE: 3.5 inch, 1.44 Mb fle
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/08/284,586
FILING DATE:
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APPLICANT: Chuntharapai, Anan
APPLICANT: Lee, James
APPLICANT: Hebert, Caroline
APPLICANT: Jin Kim, K.
           SEQUENCE CHARACTERISTICS:
LENGTH: 352 amino acids
                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/076,093A FILING DATE: 11-Jun-1993 APPLICATION NUMBER: 07/810782 FILING DATE: 19-DEC-1991 PRIOR APPLICATION DATA: APPLICATION NUMBER: 07/677211 FILING DATE: 29-MAR-1991
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                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 424
PRIOR APPLICATION DATA:
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NUMBER OF SEQUENCES:
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RESULT 5
US-08-805-478-4
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APPLICANT: Chunthal
APPLICANT: Lee, Jan
APPLICANT: Hebert,
APPLICANT: Jin Kim
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Best Local Similarity
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                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/284586
FILING DATE: 10-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/076093
FILING DATE: 11-JUN-1993
PRIOR APPLICATION DATA:
APPLICATION UMBER: 07/810782
FILING DATE: 19-DEC-1991
                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/805,478
FILING DATE: 25-Feb-1997
                         ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B.
REGISTRATION NUMBER: 34,
                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM: MEDIUM TYPE: 3.5 inc
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TELECOMMUNICATION INFORMATION:
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CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                CLASSIFICATION:
                                                                                                                                                                                                                                                                           SOFTWARE:
                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS
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              REFERENCE/DOCKET NUMBER:
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Pred. No. 6.4e-144;
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TELEPHONE:

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US-08-450-393A-6

: Sequence 6, Application US/08450393A

: Patent No. 5707815
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Matches
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APPLICANT: Charo, Israel
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INFORMATION FOR SEQ ID NO:
ATTORNEY/AGENT INFORMATION:
NAME: CSeTr, Luann
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: UCAL-237/02US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-843-5165
TELEPHONE: 415-8857-0663
                                                                                                                                                                               CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooley Godward Castro
                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT TITLE OF INVENTION: PROTEIN RECEPTORS NUMBER OF SEQUENCES: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 352 amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       301
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                                                                                                                           FILING DATE: May 25, 1995
CLASSIFICATION: 424
                                                                                                                                                                                              COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0,
                                                                                                                                                               APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                 STREET:
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mes 352; Conserva
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Amino Acid
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Pred. No. 6.4e-144;
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                                                                                                                                                                                                  Version #1.25
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; TOPOLOGY: lir; MOLECULE TYPE: ; MYPOTHETICAL: NUS-08-450-393A-6
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PCT-US95-00476-6
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SEQUENCE CHARACTERISTICS:
LENGTH: 352 amin-
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Best Local Similarity
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INFORMATION FOR SEQ ID NO:
                                                 NAME: Berliner, Robert 20,121 REGISTRATION NUMBER: 20,121 REFERENCE/DOCKET NUMBER: 55 TELECOMMUNICATION INFORMATION: 310-977-1001
                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: LEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                      SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: The Regents of the University of California TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT TITLE OF INVENTION: PROTEIN RECEPTORS
                                                                                                                                               CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
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CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                  COUNTRY: USA
ZIP: 90012-2628
                                    TELEFAX:
                                                                                                                                                                                  FILING DATE
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                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LVMGYQKKLRSMTDKYRLHLSVADLLFVITLPFWAYDAYANWYFGNFLCKAVHYIYTVNL 120
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                                    310-977-1003
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11 N. Figueroa Street, 5th F
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Pred. No. 1.5e-140;
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US-08-153-848-46
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Patent No. 5759804
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 46,
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Best Local :
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                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/977
FILING DATE: 17-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: No. 5759804and, Greta E
REGISTRATION NUMBER: 35,302
PREFERENCE DOCKET NUMBER: 37,302
                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
APPLICANT:
                                                                                                                                                                  ZIP: 60606

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                       STREET: CLICAGO
CITY: Chicago
CTATE: Illinois
TISA
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LENGTH: 352 amino acids
TYPE: amino acid
TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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               REFERENCE/DOCKET
                                                                                                                            CLASSIFICATION:
                                                                                                                                             APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE:
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les 346; Conserv
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                                                                                                                                                                                                                                                                                                                                           6300 Sears Tower,
                                                                                                                                                                                                                                                                                                                                                                                                           Gray, Patrick W.
Schweikart, Vicki L.
IVENTION: No. 5759804el Seven
EQUENCES: 64
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                                                                                                                                                                                                                                                                                                                                                             Bicknell
INFORMATION:
             NUMBER:
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98.3%;
                                                                                                                                                             US/08/153,848
                                            Greta E
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                                                                                                                                                                                                                                                                                                                                             South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                             Transmembrane
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RESULT 9
PCT-US93-11153-46
; Sequence 46, Application PC/TUS9311153
; GENERAL INFORMATION:
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Best Local Similarity
Matches 337; Conserv
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INFORMATION FOR SEQ ID NO:
                         CLASSIFICATION:
PRIOR APPLICATION DATA:
RAPPLICATION UNMBER: US 07/
APPLICATION TO THE T
                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                               SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA: APPLICATION NUMBER: PCT/US93/11153
                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 6: CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Gray, Patrick W. APPLICANT: Schweikart, Vicki L.
                                                                                                                                                                                                                                                                                      STREET: Chicago
                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
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TELEFAX: (
TELEX: 25-
                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                       COUNTRY: UZIP: 60606
                                                                                                                  FILING DATE:
 REGISTRATION NUMBER:
                 NAME:
                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Marshall, O'Toole,
ADDRESSEE: Bicknell
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                 Noland,
                                                                                                                                                                                                                                                                                         Illinois
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(12) 474-0448
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35,302
                                                                  07/977,452
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RESULT 10
US-07-759-568-1
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Patent No. 5374506
GENERAL INFORMATION:
APPLICANT: Murphy, Philip M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity Matches 337; Conserv
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TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 337 amino acids
                                  APPLICATION NUMBER: US/07/75
FILING DATE: 19910913
CLASSIFICATION: 435
ATTORNEY_AGENT INFORMATION:
NAME: Scott, Watson T.
REGISTRATION NUMBER: 26581
                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
REFERENCE/DOCKET NUMBER: WITELECOMMUNICATION INFORMATION:
                                                                                                                                                          SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Murphy, Philip M.
TITLE OF INVENTION: Cloning of cDNA Encoding a Functional
TITLE OF INVENTION: Human Interleukin-8 Receptor
NUMBER OF SEQUENCES: 5
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               196 VVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKALKTTVILILAFFACWLPY 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          316
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                                                                                                                                                                                                                                                                                                                                                  CITY: Washington
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1615 L Street,
                                                                                                                                                                                                                                                                                                             USA
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                                                                                                                                             US/07/759,568
                                                                                                                                                                                                                                                                                                                                                                       Darby & Cushman
et, N.W.
                   WTS/5683/91535/WBH
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RESULT 11
US-08-202-056-7
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 355 amino acids
TYPE: AMINO ACID
STRANDENNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 7, Application US/08202056 Patent No. 5440021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 31.0%;
Best Local Similarity 35.3%;
Matches 132; Conservative 6
                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
                           SOFTWARE: patin (Genentech)
CURRENT APPLICATION NUMBER: US/08/202,056
APPLICATION NUMBER: US/08/202,056
                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech,
                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: Antibodies NUMBER OF SEQUENCES: 8
                                                                                                                                                                                                                                                                                                                                            APPLICANT: Kim, Kyung Jin APPLICANT: Lee, James
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       339
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                                                                                                                                                                                                        STREET: 460 Point San Bruno CITY: South San Francisco STATE: California
FILING DATE: 2: CLASSIFICATION:
                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 62 SLVMLVILYSRVGRSVTDVYLLNLALADLLFALTLPIWAASKVNGWIFGTFLCKVVSLLK 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SRPSFVGSSSGHTS 352
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ----ANVSEADDRYICDRFYPNDL--WVVVFQFQHIMVGLILPGIVILSCYCIIISKLSH 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EVNFYSGILLLACISVDRYLAIVHATRTLTQKRYLV-KFICLSIWGLSLLLALPVLLFRR 180
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Hebert, Caroline
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                   25-FEB-1994
                                                                                            PC-DOS/MS-DOS
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                                                                                                                               360 Kb floppy disk
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Pred. No. 6.7e-40;
59; Mismatches 119; Indels
                                                                                                                                                                                                                                                  Blvd
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PatentIn Release #1.0, Version #1

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US-08-450-393A-8
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                                                                                                                                                                                                                                                                                                        Sequence 8, Application US/08450393A Patent No. 5707815
GENERAL INFORMATION:
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TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
ZIP: 94306-2155
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                   APPLICANT: Charo, Israel
APPLICANT: Coughlin, Shaun
TITLE OF INVENTION: MANWALLAN MONOCYTE CHEMOATTRACTANT
TITLE OF INVENTION: PROTEIN RECEPTORS
NUMBER OF SEQUENCES: 14
                                                                                          STREET: STREET: STREET: Palo Alto CITY: Palo Alto CITY: California
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APPLICATION NUMBER: 07/67
FILING DATE: 29-MAR-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                         CORRESPONDENCE ADDRESS
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                                                                                                                                                                           ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ILGILHSCLNPLIYAFIGQKFR----HGL-----LKILAI-----HGLISKDSLPKD 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ALAFFHCCLNPILYAFLGAKFKTSAQHALTSVSRGSSLKILSKGKRGGHSSVSTES----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ----ANVSEADDRYICDRFYPNDL--WVVVFQFQHIMVGLILPGIVILSCYCIIISKLSH 228
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RESULT 13
PCT-US95-00476-8
; Sequence 8, Application PC/TUS9500476
; GENERAL INFORMATION:
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; HYPOTHETICAL: NO
US-08-450-393A-8
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Matches 132;
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COUNTRY: USA
ZIP: 90012-2628
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                   APPLICANT: The Regents of the University of California TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT TITLE OF INVENTION: PROTEIN RECEPTORS
                                                                                                                                                  NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: 415-843-5165
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn Rel CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                            345
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            181 TVYSSNVSPA-----CYEDMGNNTANWRMLLRILPQSFGFIVPLLIMLFCYGFTLRTLFK 235
                                                                                          ADDRESSEE: Robbins, Berliner & Carson STREET: 201 N. Figueroa Street, 5th FCITY: Los Angeles
                                                                             STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          57 GLVILVMGYQKKLRSMTDKYRLHLSVADLLEVITLPFWAVDAVANWYFGNFLCKAVHVIY 116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62 SLVMLVILYSRVGRSVTDVYLLNLALADLLFALTLPIWAASKVNGWIFGTFLCKVVSLLK 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER: 31,822
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                                                                                                                                                                                                                                                                                                                                                                              -----ESSSFHSS 352
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              ALAFFHCCLNPILYAFLGAKFKTSAQHALTSVSRGSSLKILSKGKRGGHSSVSTES----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SKGHQKRKALKTTVILILAFFACWLPYYIGISIDSFILLEIIKQGCEFENTVHKWISITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ----ANVSEADDRYICDRFYPNDL--WVVVFQFQHIMVGLILPGIVILSCYCIIISKLSH 228
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                                                                         California
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25, 1995
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Pred. No. 6.7e-40;
9; Mismatches 119
                                                                                                                5th Floor
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11;

SOFTWARE: Patentin Rel CURRENT APPLICATION DATA:

OPERATING SYSTEM: PC-DOS/MS-DOS

Release #1.0,

Version

#1.25

IBM PC compatible

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RESULT 14
US-08-202-056-1
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                         GENERAL INFORMATION:
APPLICANT: Chuntharapai, Anan
APPLICANT: Hebert, Caroline
APPLICANT: Kim, Kyung Jin
APPLICANT: Lee, James
ITITLE OF INVENTION: Antibodies to Hu
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PCT-US95-00476-8
                                                                                                                                                                             Sequence 1, Application US/08202056 Patent No. 5440021
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 355 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
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HYPOTHETICAL:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 310-977-1001
TELEFAX: 310-977-1003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              175
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                 STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EVNFYSGILLLACISVDRYLAIVHATRTLTQKRYLV-KFICLSIWGLSLLLALPVLLFRR 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SDSFEDFWKGEDLSNYSYSSTLPPFLLDAAPC-EPESLEINKYFVVIIYALVFLLSLLGN 61
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                                                                                                                                                                                                                                                                                                             -----ESSSFHSS 352
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South San Francisco
               460 Point San Bruno
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5555-291
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Pred. No. 6.7e-40;
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                                                                                Human
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                                                                              Type
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                                                                                                                                                 Sequence 2, Application US/08076093A Patent No. 5543503 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local
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TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/677
FILING DATE: 29-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: LOVE, RICHARD B.
REGISTRATION NUMBER: 34,65
REFERENCE/DOCKET NUMBER: 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
                 APPLICANT: Jin Kim, K. TITLE OF INVENTION: AN NUMBER OF SEQUENCES: 6 CORRESPONDENCE ADDRESS:
                                                                         APPLICANT: Chuntharapai, Ana
APPLICANT: Lee, James
APPLICANT: Hebert, Carroline
APPLICANT: Jin Kim, K.
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LENGTH: 350 amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   71 SMTDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNLYSSVLILAFI 130
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TELEFAX: 415/952-9881
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11 NYTEEMGSGDYDSMKEPCFREENANFNKIFLPTIYSIIFLTGIVGNGLVILVMGYQKKLR 70
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les 121; Conservative
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 ADDRESSEE:
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amino acid
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Genentech,
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                                   Antibodies 6
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Pred. No. 4.9e-39;
66; Mismatches 127;
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                                                     Human PF4A Receptors
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CLASSIFICATION: JOE CLASSIFICATION DATA:
APPLICATION NUMBER: 07/810782
FILING DATE: 19-DEC-1991
PRIOR APPLICATION DATA: 19-DEC-1991
PRIOR APPLICATION DATA: 19-DEC-1991
PRIOR APPLICATION NUMBER: 07/677211
APPLICATION NUMBER: 29-MAR-1991
FILING DATE: 29-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: LOVE, RICHARID STATEMENT OF THE TOWN WHORE 34,659
REGISTRATION NUMBER: 706P2
FELECOMMUNICATION INFORMATION: 15-25-550
FELECOMMUNICATION INFORMATION: 415/925-9881
FELEPAX: 415/927-9881
FELEPAX: 415/927-9881
FELEPAX: 910/371-7168
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 350 amino acids
TOPDLOGY: Linear
US-08-076-093A-2
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Search completed: September 14, 1999, 09:51:01 Job time: 46 sec
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COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTMARE: WinPatin (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/076,093A

FILING DATE: 11-Jun-1993

CLASSIFICATION: 530
                                                                                                                                                                  191 LGNDTAKWRMVLRILPHTFGFIVPLFVMLFCYGFTLRTLFKAHMGQKHRAMRVIFAVVLI 250
                                                                                                                                                                                                                                                                                 190 YPNDL--WYVYFQFQHIMYGLILPGIVILSCYCIIISKLSHSKGHQKRKALKTTVILILA 247
                                                                                                                                                                                                                                                                                                                     132 SVDRYLAIVHATRTLTOKRHLV-KFVCLGCWGLSMNLSLPFFLFRQAYHPNNSSPVCYEV 190
                                                                                                                                                                                                                                                                                                                                             308 KF-----KTSAQHALTS 319
                                                                                            311 NFRHGFLKILAMHGLVS 327
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CITY: South San Francisco
STATE: California
COUNTRY: USA
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Human G-protein ch African green monk

Run on: OM protein - protein search, using sw model September 14, 1999, 09:50:15; Search time 14.3 Seconds (without alignments) 583.043 Million cell updates/sec GenCore version 4.5 Copyright (c) 1993 - 1998 Compugen Ltd.

Title: Perfect score: US-09-104-063-4 1830

1 MEGISIYTSDNYTEEMGSGD......KRGGHSSVSTESESSSFHSS 352

Scoring table: BLOSUM62

Searched: 188963 seqs, 23686106 residues

Database : A_Geneseq_36:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

43	42	41	40	39	38	37	36	35	34	ω	32	31 1	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12		10	9	œ		6	5	4	ω	2	1	NO.	Pocul+
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G-prot	MCP-4 rec	ā	Вa	G-protein coupled	വ	kine superfa	an lymphocyte	elet f	nce in a low		membra	Murine V31 seven t	transmembr	3	tide seque	Partial sequence o	ven tr	ב	Interleukin 8 rece	1-0	-8 rec	Recombinant high a	in-8 r	ven tr	nt hi	ice in a hi	tei	leukin 8 re	·8 rec	uence in	type 2-GBP	binant high	IP-10/Mig r	odent che	nemokine	ine	transmembr	3	rotein cou	ew platele	kine superfa	mono	scription	

RESULT 2 R80757 ID R80757 AC R80757; DT 26-MAR-

R80757 standard: Protein; 352 AA. R80757; 26-MAR-1996 (first entry)

ALIGNMENTS 861212 standard; Protein, 352 AA. 8681212 standard; Protein, 352 AA. 868123 standard; Protein, 36812 and 86813. 868123 standard; Protein, 352 AA. 868123 standard; Protein, 36812 and 86813. 868123 standard; Protein, 352 AA. 868123 standard; Protein, 36812 and 86813. 86813 standard; Protein, 36812 and 86813. 86812 standard; Protein,	Дb	Db	Qy	B &) L	. Q	2 5	Z 29	ρb	Qy	Que Bes Mat	SQ													PN	O K	KW	K W	DE	2		RESUI R6881	
	OI LYAFIGAKFKTSAOHALTSVSRGSSIKIIJSKGKRGGHSSVSTESESSSFHSS 35		41 TVILILAFFACWLPYYIGISIDSFILLEIIKOGCEFENTVHKWISITEALAFFHCCLNPI	DDRYICDREYENDLWYVFORQHIMYGLILFGIVILSCYCIIISKLSHSKGHOKRALKT	1 SSVLILAFISLDRYLAIVAATNSQRPRKLLAEKVYYVGVWIPALLLTIPDSTFANVSEA 18	*SSVELLAF1SLDRYLAIVHAINSQRPXXLLAEXVYYVGVW1PALLLTIPDF1FANVSEA 18	TO SEE THE SECOND SECON	1 LVMGYQXKLRSYTDKYRHHSYADLLEVITLPEWAYDAVANWYEGNELCKAVHVIYTVNL 12	MEGISIYTSDNYTEEMGSGDYDSMKEPCFREENANFNKIFLPTIYSIIFLTGIVGNGLVI 60	MEGISIYTSDNYTEEMGSGDYDSMKEPCFREENANFNKIFLPTIYSIIFLTGIVGNGLVI 6	atch 100.0%; Score 1830; DB 1; Length 352; cal Similarity 100.0%; Pred. No. 2.1e-212; 352; Conservative 0; Mismatches 0; Indels 0; Gaps	Sequence 352 AA;	en in Q80521 and Q80522, and their respect	in Q80520). The nucleotide sequences of the	ing a large fragment of IL-8 receptor DNA (fo	s were identified by probing lambda libraries fr	ge 54-56; 83pp; English.	eptide	mmatory disorders - by administering an	N-PSDB; Q80521.	ebert C, Kim KJ, Lee J	INC.	6093	22-DEC-1994.	W09428931-A.	peutic.	nphysema; cysti	hemotacti	Human monocyte PF4AR.	18-JUL-1995 (first entry)	R68812 standard; Protein; 352 AA. R68812:	0017 1 1812	ALIGNMENTS

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Best Local s
Matches 352
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Antibodies directed against the interleukin-8 receptor B can be used to treat or prevent inflammation e.g. psoriasis, dermatitis, to treat or prevent inflammation e.g. psoriasis, dermatitis, rheumatoid arthritis and particularly inflammatory bowel disease and check interleukin-8 receptor B expression in cells and tissues and for affinity purification of interleukin-8 receptor B from cells. This sequence is an additional chemokine superfamily receptor which was identified by probing lamda libraries of genomic DNA from a human monocyte-like cell line (L-60) and human peripheral blood lymphocytes using a large fragment of the interleukin-8 type as receptor DNA (See Q99006).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29-MAR-1991; 677211.
29-MAR-1991; US-677211.
25-FEB-1994; US-202056.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               chronic lung inflammation; treatmaffinity purification; detection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chemokine superfamily receptor.
Interleukin; IL-8; inflammation; psoriasis; dermatitis; rheumatoid arthritis; inflammatory bowel disease; rheumatoid arthritis; inflammatory bowel disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   or prevent inflammation,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chuntharapai A, H
WPI; 95-283151/37.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New antibodies against interleukin
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12-MAR-1993 (first entry)
New platelet factor 4 receptor superfamily member PF4AR1.
IL-8R: G-protein coupled receptor family; rhodopsin super
pro-inflammatory cytokine; 8rr.20.15.
                                        R27792;
12-MAR-1993
                                                                 R27792
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                                                                                                                              MEGISIYTSDNYTEEMGSGDYDSMKEPCFREENANFNKIFLPTIYSIIFLTGIVGNGLVI
                                                                                                                                                                                                                                YSSVLILAFISLDRYLAIVHATNSQRPRKLLAEKVVYVGVWIPALLLTIPDFIFANVSEA
                                                                                                                                                                                                                                                                                                                                                   TVILILAFFACWLPYYIGISIDSFILLEIIKQGCEFENTVHKWISITEALAFFHCCLNPI
                                                                                                                                                                                                                                                                                                                                       LVMGYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNL
                                                                                                                                                                                                                                                                                    YSSVLILAFISLDRYLAIVHATNSQRPRKLLAEKVVYVGVWIPALLLTIPDFIFANVSEA
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                                                                 standard;
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52; Conservative
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                                                                 Protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 1830; DB 1; 100.0%; Pred. No. 2.1e-212;
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                 superfamily;
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Best Local S
Matches 351
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Isolated human platelet fa polypeptide and corresp. a diagnostic and screening a pr4AR-mediated disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
W09217497-A.
15-OCT-1992.
23-MAR-1992; U02317.
29-MAR-1991; US-677211.
19-DEC-1991; US-810782.
(GETH) GENENTECH INC.
Holmes WE, Lee J, Wood WI
WPI; 92-366101/44.
                                                                                                                                                                                                                                                                                                                                                                                        The II-8 receptor CDNA sequence was isolated (see Q29505) and a 874bp sub-fragment of the coding sequence was used as a probe to screen human cell line HI60 and human peripheral blood lymphocyte cDNA libraries. Two new gene sequences were found that are clearly related to the II-8 receptor. One of these was contained in combined clone 8rr.20.15 and is predicted to encode an amino acid sequence which is 34% identical with both the high and low affinity II-8 receptors. See also Q37107.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 7; Fig 4; 78pp; English. The IL-8 receptor cDNA sequence
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                        301
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                                                 LVMGYOKKLRSMTDKYRLHLSVADLLFVITLÞFWAVDAVANWYFGNFLCKAVHVIYTVNL 120
                                                                                                                                                                                                                                                                       MEGISIYTSDNYTEEMGSGDYDSMKEPCFREENANFNKIFLPTIYSIIFLTGIVGNGLVI
LYAFLGAKFKTSAQHALTSVSRGSSLKILSKGKRGGHSSVSTESESSSFHSS
                  LYAFLGAKFKTSAQHALTSVSRGSSLKILSKGKRGGHSSVSTESESSSFHSS
                                                                                                        DDRYICDRFYPNDLWVVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKALKT
                                                                                                                                                            YSSVLILAFISLDRYLAIVHATNSQRPRKLLAEKVVYVGVWIPALLLTIPDFIFANVSEA
                                                                                                                                                                            YSSVLILAFISLDRYLAIVHATNSQRPRKLLAEKVVYVGVWIPALLLTIPDFIFANVSEA
                                                                                                                                                                                                                  LVMGYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNL
                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                          99.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             factor 4 super-family antibodies and DNA -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               agents,
                                                                                                                                                                                                                                                                                                                            score 1819; D. Pred. No. 4.5e 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                and for treating inflammation or
                                                                                                                                                                                                                                                                                                                                            DB 1;
..5e-211;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             receptor
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W97362
W97362 standard; Protein; 356 AA.

RESULT
W97362
C w97362;
DI 12-MAY-1999 (first entry)
DE G-protein coupled receptor polypeptide designated CXCR4B.
C encert coupled receptor; CXCR4B; human; splice variant;
C encert pain; diabetes; obesity; anorexia; bullmia; asthma;
C ancer; pain; diabetes; acute heart failure, hypotension; hypertension;
C wrinson's disease; acute heart failure, hypotension; hypertension;
C wrinary retention; osteoporosis; angina pectoris; myocardial infarction;
C wrinary retention; osteoporosis; angina pectoris; myocardial infarction;
C wrinary retention; osteoporosis; angina pectoris; myocardial infarction;
C wrinary retention; osteoporosis; angina destriction; myocardial infarction;
C wrinary retention; osteoporosis; angina destricti
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24-JUL-1998; 20-AUG-1997; 07-AUG-1998;

US-056601. US-056601.

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RESULT
W48734
ID W4
AC W7
DT 2!
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KW V1
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CC The present sequence represents a G-protein coupled receptor polypeptide contains a human splice variant of a chemokine receptor CXCR4B, which is a human splice variant of a chemokine contains a susceptibility to diseases by detecting mutations or contains a susception of cancer and polypeptides and polypeptides are useful for contains of cancer also useful for screening for the presence or amount of caponists which can be used to treat conditions associated with CXCR4B colypeptide imbalance. CXCR4B polypeptides can be administered directly (as a vaccine) or via a vector (gene therapy) to prevent disease.

CC Diseases diagnosed, prevented and treated include: HIV-1 and HIV-1 (as a vaccine) or via a vector (gene therapy) to prevent disease.

CC Parkinson's disease; acute heart failure; hypotension; hypertension; curinary retention; osteoprosis; angina pectoris; myocardial infarction; crantaitor, osteoprosis; angina pectoris; myocardial infarction; crantaitor, solvension; benign prostatic hypertrophy, migraine; continued the syndrome. CXCR4B polypeptides are useful for mapping genes continued the syndrome. CXCR4B polypeptides are useful for mapping genes continued contromosomes, allowing gene inheritance to be studied through linkage can be continued through linkage and contents and co
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Best L
w48734;
25-SEP-1998 (first entry)
Human RM3 seven transmembrane (7TM) receptor.
V28; placenta; seven transmembrane receptor;
V38; placenta; seven transmembrane receptor;
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N-PSDB; X15882.
                                                                                                         W48734 standard;
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                                                                                                                                                                                                                                       FLGAKFKTSAQHALTSVSRGSSLKILSKGKRGGHSSVSTESESSSSFHSS 352
                                                                                                                                                                                                                                                                                               ISIYTSDNYTEEMGSGDYDSMKEPCFREENANFNKIFLPTIYSIIFLTGIVGNGLVILVM 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GYQKKLRSMTDKYRLHLSVADLLEVITLPEWAVDAVANWYFGNELCKAVHVIYTVNLYSS 123
                                                                                                                                                                                                              FLGAKFKTSAQHALTSVSRGSSLKILSKGKRGGHSSVSTESESSSFHSS
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Pred. No. 9.6e-210;
1; Mismatches 1;
                                                                                                       A
                    receptor; 7TM; signal transduction;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PT DNA encoding v28 seven transmembrane receptor polypeptide - useful producing recombinant polypeptide and antiv28 antibodies, and producing recombinant polypeptide and antagonists and producing recombinant polypeptide and antagonists and producing recombinant polypeptide and antagonists and producing the producing sasays for v28 agonists and antagonists.

The present sequence represents the human RM3 protein which is encoded by the full length genomic RM3 clone (V18357) which was isolated from a human macrophage cDNA library. The invention claims for the full clength v28 genomic DNA sequence (V1835) isolated from a human placenta genomic library. The v28 (W48722) and RM3 proteins are seven transmembrane (77M) receptors which are probably involved in signal transmembrane (77M) receptors which are probably involved in signal transmembrane to produce the recombinant polypeptide, to produce anti-v28 antibodies or in screening assays for v28 agonists or antagonists. The antibodies, agonists and antagonists could then be used to modulate v28 receptor-ligand binding, for e.g. in immunological and/or inflammatory events in vivo.

Sequence 337 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
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Best Local
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Godiska R, Gray PW, Schweickart
WPI; 98-332132/29.
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                                 ALTSVSRGSSLKILSKGKRGGHSSVSTESESSSFHSS
                                                                                                                                        YIGISIDSFILLEIIKQGCEFENTVHKWISITEALAFFHCCLNPILYAFLGAKFKTSAQH
                                                                                                                                                                                                                           LAIVHATNSQRPRKLLAEKVVYVGVWIPALLLTIPDFIFANVSEADDRYICDRFYPNDLW
                                                                                                                                                                                                                                                                                                                                                                             LAIVHATNSQRPRKLLAEKVVYVGVWIPALLLTIPDFIFANVSEADDRYICDRFYPNDLW 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YRLHLSVADLLEVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNLYSSVLILAFISLDRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MGSGDYDSMKEPCFREENANFNKIFLPTIYSIIFLTGIVGNGLVILVMGYQKKLRSMTDK
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   ALTSVSRGSSLKILSKGKRGGHSSVSTESESSSFHSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                               YRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNLYSSVLILAFISLDRY
                                                                                                             YIGISIDSFILLEIIKQGCEFENTVHKWISITEALAFFHCCLNPILYAFLGAKFKTSAQH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                95.7%; Score 1752; DB 1; ilarity 100.0%; Pred. No. 5.1e-203; Conservative 0; Mismatches 0;
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US-977452.
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287. .3
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17-NOV-1993; U11153
17-NOV-1992; US-977452.
(ICOS-) ICOS CORP.
GOdiska R. Gray PW. Sc
WPI: 94-200264/24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        prods. for use as therapeutic or diagnostic agents for conditions involving the receptors.

Example 11: Page 84-85: 100pp: English
Two primers (066148, 066149) were used in a PCR reaction containing human macrophage cDNA library in plasmid pRC/CMV. When the PCR products were subjected to agarose gel electrophoresis a faint band of 180-200 base pairs was observed. Re-amplified material was digested with BanHI and HindIII and cloned into the plasmid Bluescript SK- Of sixteen clones sequenced, two contained a unique sequence termed RM3. Specific primers for the partial RM3 clone were used to identify a full length RM3 CDNA clone (066179) which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA encoding seven trans:membrane receptors prods. for use as therapeutic or diagnostic
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337 AA;
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115. 13
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287. .31
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198. .2
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159. .1
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07-FEB-1997; W0-J00299.
(SHIO) SHIONOGI & CO LT
IIZASA H, KISHIMOTO T, N
YOSHIDA N, YOSHIE O;
WPI; 98-447232/38.
       Chemokine receptor K5.5; MIP-1-alpha; atheroma; HIV; AIDS; graft rejection;
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R99274;
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Sequence
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13-AUG-1998.
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N-PSDB; V46370.
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                                                                                                                                                                                                                                                                                                                                  GYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAMADWYFGKFLCKAVHIIYTVNLYSS 125
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Pred. No. 4.1e
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                      allergy;
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WO9623068-A1. 01-AUG-1996. 24-JAN-1996; G00143. 27-JAN-1995; GB-001683.

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Claim 1: Fig 3: 47pp: English.

Claim 2: Fig 3: 47pp: English.

Claim 2: Fig 3: 47pp: English.

Claim 3: Fig 3: 47pp: English.

Claim 4: Fig 3: 47pp: English.

Claim 6: Fig 4: 47pp: Engli
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20-007-1998 (first entry)
20-007-1998 (first entry)
Rodent chemokine receptor HST01.1 amino acid sequence.
Rodent chemokine receptor; asthma;
Chemokine, primate; human; rodent; chemokine receptor; asthma;
Chemokine, primate, primate; force;
inflammatory response; immune response; leukocyte migration; GPCR;
leukocyte adhesion; chemoattractant; modulation; antiviral response;
cellular morphology modification response; G-protein coupled receptor;
cellular morphology modification response;
cellular morphology modification; response;
cellular morphology modification;
cellular 
                                                                                                                                                                                             30-JUL-1998.
22-JAN-1998: U00902.
23-JAN-1997: US-036715.
35CHE ) SCHERING CORP.
Gorman DM, Hedrick JA, Mattson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            W69999 standard; Protein; 367
                                                                                                                                                                                                                                                                                                                                                                                                                                             MUS SP.
WO9832858-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               atrophy; HST01.1
                                                   WPI; 98-427954/36.
N-PSDB; V43793.
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                                                                                                                                                         Zlotnik A;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKALKTTVILILAFFACWLPYYIG
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          and primate chemokines
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39.4%;
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Pred. No. 1.1e-63;
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                              chemokine receptors
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This represents a rodent chemokine receptor HST01.1 amino acid sequence. The invention provides novel primate and rodent chemokines and chemokine compounds (optionally receptors. The chemokines, receptors and binding compounds (optionally receptors. The chemokines, receptors and binding compounds (optionally contibodies/fragments specifically binding the chemokines) are useful contibodies/fragments specifically binding the chemokines are useful conditions associated with abnormal physiology therapeutically to treat conditions associated with abnormal physiology or development e.g. inflammatory conditions such as asthma. Chemokines are important in immune and inflammatory responses in that they induce conditions such as asthma. Chemokines are important in immune and almamatory responses in that they induce conditions are also chemoattractants for consistent cells involved in inflammation and can induce other biological several cells involved in inflammation and can induce other biological cesponses e.g. modulation of second messenger levels (e.g. Ca++), conceptors of chemokine and chemokine responses et. The chemokine receptors of the invention exhibit structural properties of G-protein coupled conceptors (GPCR), although their ligands have not yet been identified. Conceptors (GPCR), although their ligands have not yet been identified. Consideration exhibits the receptor polypeptides are useful to produce themokine receptor polypeptides are useful to produce complexes in vivo or in assay techniques. Assays may considered to produce the physiological responses in cells can be used to modulate the physiological responses in cells can also used to produce antibodies useful diagnostically, for drug care also used to produce antibodies useful diagnostically, for drug care also used to produce antibodies useful diagnostically, for drug care also allow transformation of cells for polypeptides, and to isolate the polypeptides or related sequences, especially from other species. They also allow transformation of cells fo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QΥ
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RESULT W5437LI W54437LI W102 W102 LI CONTROL C
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Best Local
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                                                                                                                                       Human IP-10/Mig receptor CXCR3 protein chemokine receptor; cellular signal; tantiviral; inflammatory disease
                                                                                                                                                                                                                                              14-AUG-1998 (first entry)
                                                                                                                                                                                                                                                                                                               W54371 standard; Protein; 368
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                                                                                                          Homo sapiens.
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                                           Modified_site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REKMWMLFTRLGRSD-----QRGPQRQPSSSRRESSW
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                                                                         Location/Qualifiers
          /note=
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          "N-linked glycosylation
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pred. No. 2.6e-61;
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                                                                                                                                                                                          treatment; T cell;
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                             site"
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10-SEP-1996; US-709838.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Monoclonal antibody against recombinant II-8 receptor polypeptide useful for treating inflammatory disorders, for detecting neutrophil(s) and for isolating II-8 receptor from liq.mixt. Claim 5; Fig 4A-B; 74pp; English I.

Claim 5; Fig 4A-B; 74pp; English II-8 receptor structure in the receptor structure in the receptor from liq.mixt.

Monoclonal antibodies were raised against recombinant interleukin-8 (II-8) receptor subtypes A and B from both human and rabbit sources (R80950-53 encoded by 099949-52). The A subtype receptor (II-8rA) is a high affinity receptor and the B subtype receptor (II-8rB) is a high affinity receptor and the B subtype receptor (II-8rB) is a low affinity receptor. The monoclonal antibody (mAb) pref. binds to the II-8 binding domain thus blocking its activation. The mabs are useful for treating inflammatory disorders (see key words) and for detecting the presence of neutrophils in a biological sample. The mabs are also useful in the isolation of II-8 receptors from a mixture.
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15-MAR-1994; US-210250.
02-MAY-1994; US-237937.
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                                                                                                                                                                                                                                                                                                         ILGILHSCLNPLIYAFIGQKFR---
                                                                                                                                                                                                                                                                                                                                                              ALAFFHCCLNPILYAFLGAKFKTSAQHALTSVSRGSSLKILSKGKRGGHSSVSTES----
                                                                                                                                                                                                                                                                                                                                                                                                                            AHMGQKHRAMRVIFAVVLIFLLCWLPYNLVLLADTLMRTQVIQETCERRNHIDRALDATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SKGHQKRKALKTTVILILAFFACWLPYYIGISIDSFILLEIIKQGCEFENTVHKWISITE 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TVYSSNVSPA-----CYEDMGNNTANWAMLLAILPQSFGFIVPLLIMLFCYGFTLRTLFK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----NVSEADDRYICDRFYPNDL--WVVVFQFQHIMVGLILPGIVILSCYCIIISKLSH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SDSFEDFWKGEDLSNYSYSSTLPPFLLDAAPC-EPESLEINKYFVVIIYALVFLLSLLGN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         standard; Protein;
                                                                                                                                                                                                                                              ESSSFHSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              360 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Larosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Navarro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 574; DB 1;
Pred. No. 7.8e-61;
7; Mismatches 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         æ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                120;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                         -HGLISKDSLPKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           360;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hybrid peptides for binding cycokines, comprising a malaria parasite CP Plasmodium falciparum) peptide (capable of binding to a red blood CC cell (RBC)) and a receptor peptide are claimed. R70103-25 are examples CC of these hybrid peptides. R70124 is a fusion of interleukin 8 receptor CC type 2 and glycophorin binding protein (GBP) 130. The use of cytokine CC receptors not normally found on RBCs means that the cytokine can bind CC harmlessly to the RBC without deleterious effect. The RBC protects the CC hybrid peptides from excretion from the kidney, and due to steric CC hindrance prevents the cytokines binding to a receptor in another cell. CC GBP 130 or GBPH (GBP homologue) are the prefid. malaria parasite peptides used, others include EBA 175 (175 kDa erythrocyte binding antigen), CC receptor molecule (eg. exhibited by plasmodium vivax). These peptides CC bind to pref. glycophorin A, B and C, sialo glycoptoteins, found on the surface of RBCs. The hybrid peptides are thus used to lower the levels of free cytokines in the circulation to reduce pathological
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 35.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               09-MAR-1995
01-SEP-1994; G01900.
03-SEP-1993; GB-018350.
23-AUG-1994; GB-017021.
(PREN/) PRENDERGAST K F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               red blood cell; cytokine recept GBP 130; GBPH; glycophorin bind Chimeric Plasmodium falciparum. W09506737-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14-FEB-1996 (first entry)
IL8-R type 2-GBP 130 fusion protein.
Hybrid peptide; malaria parasite; Plasmodium falciparum; fusion protein; red blood cell; cytokine receptor; glycophorin binding peptide 130; caph: glycophorin binding peptide homologue; glycophorin A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             a receptor peptide.
Example A; Page 80-82; 93pp; English.
Hybrid peptides for binding cytokines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New hybrid peptide(s) for binding malaria parasite peptide capable of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
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WPI; 95-115452/15
339
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                                                                                                                                                                             KGHQKRKALKTTVILILAFFACWLPYYIGISIDSFILLEIIKQGCEFENTVHKWISITEA
                                                                                                                                                                                                                                                                                                                                  VNLYSSVLILAFISLDRYLAIVHATNSQRPRKLLAEKVVYVGVWIPALLLTIPDFIF---
                                                                                                                                                                                                                                                                                                                                                                                                                LVILVMGYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYT 117
                                                                                                                                                   HMGQKHRAMRVIFAVVLIFLLCWLPYNLVLLADTLMRTQVIQETCERRNHIDRALDATEI
                                                                                                                                                                                                                                                                       ---ANVSEADDRYICDRFYPNDL--WVVVFQFQHIMVGLILPGIVILSCYCIIISKLSHS
                                                                                                                                                                                                                                                                                                                                                                                         LVMLVILYSRVGRSVTDVYLLNLALADLLFALTLPIWAASKVNGWIFGTFLCKVVSLLKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SDSFEDFWKGEDLSNYSYSSTLPFLLDAAPC-EPESLEINKYFVVIIYALVFLLSLLGNS 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SDNYT-----EEMGSGDYDSM-----KEPCFREENANFNKIFLPTIYSIIFLTGIVGNG 57
                                      ----ESSSFHSS
                                                                           LGILHSCLNPLIYAFIGQKFR---
                                                                                                                LAFFHCCLNPILYAFLGAKFKTSAQHALTSVSRGSSLKILSKGKRGGHSSVSTES-----
                                                                                                                                                                                                                                                                                                            VNFYSGILLLACISVDRYLAIVHATRTLTQKRYLV-KFICLSIWGLSLLLALPVLLFRRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1064 AA;
                                                                                                                                                                                                                                -CYEDMGNNTANWRMLLRILPQSFGFIVPLLIMLFCYGFTLRTLFKA
                                    352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 568.5; DB 1;
Pred. No. 1.8e-59;
9; Mismatches 119;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g cytokine(s) of binding a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        s) - comprising a
a red blood cell and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 1064;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                           -HGLISKDSLPKDS
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CRabbit high affinity IL-8 receptor gene was isolated from rabbit peritoneal neutrophils and used as a source of poly(A)+ RNA, to produce a rabbit neutrophil cDNA library. 250,000 recombinant produce a rabbit neutrophil cDNA library. 250,000 recombinant produce a rabbit neutrophil cDNA library. 250,000 recombinant produce derived from those which hybridized to an antisense oligonucleotide (030015). This probe was designed based on the coupled receptors. After tertiary screening, six plaques were coupled receptors. After tertiary screening, six plaques were isolated. The insert of one of these plaques, termed F3R was of 2.5 kb in size. This insert was sequenced. The protein deduced from the F3R clone demonstrates that it belongs to the family of corpotein-coupled receptors. The deduced protein sequence indicates seven putatuve transmembrane segments. A human peripheral blood leukocyte lambda gtll cDNA library (5' stretch) was screened with a 652 bp EcoRI/BamHI fragment (including nucleotides 2.7 to 625) of the rabbit F3R clone. After tertiary screening several human clones which hybridized to the rabbit IL-8 probe were isolated. The insert of one such clone, termed 4AB was sequenced (330012).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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10-APR-1992; U02977.
10-APR-1991; US-685101.
09-JUL-1991; US-726606.
09-DEC-1991; US-803842.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sequenced
Sequence
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(UYBO-) UNIV BOSTON.
Navarro J, Thomas KM, 1
WPI; 92-382123/46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence in a low affinity recombinant human interleu (IL-8) receptor polypeptide in 4AB.
IL-8 receptor polypeptide; G-protein-coupled receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Recombinant mammalian interleukin-8 receptor - used for screening interleukin-8 binding antagonists, used to treat inflammation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
WO9218641-A.
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04-APR-1993
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                                                                     301
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hes 132;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TVNLYSSVLILAFISLDRYLAIVHATNSQRPRKLLAEKVVYVGVWIPALLLTIPDFIF---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SLVMLVILYSRVGRSVTDVYLLNLALADLLFALTLPIWAASKVNGWIFGTFLCKVVSLLK 126
                                                                     ILGILHSCLNPLIYAFIGQKFR----HGL---
                                                                                                                                                                                                                                                                           SKGHQKRKALKTTVILILAFFACWLPYYIGISIDSFILLEIIKQGCEFENTVHKWISITE
                                                                                                                                                                                                                                                                                                                                                TVYSSNVSPA-----CYEDMGNNTANWRMLLRILPQSFGFIVPLLIMLFCYGFTLRTLFK
                                                                                                                                                                                                                                                                                                                                                                                                              ----ANVSEADDRYICDRFYPNDL--WVVVFQFQHIMVGLILPGIVILSCYCIIISKLSH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EVNFYSGILLLACISVDRYLAIVHATRTLTQKRYLV-KFICLSIWGLSLLLALPVLLFRR 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GLVILVMGYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIY 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SDSFEDFWKGEDLSNYSYSSTLPPFLLDAAPC-EPESLEINKYFVVIIYALVFLLSLLGN
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                                                                                                                                   ALAFFHCCLNPILYAFLGAKFKTSAQHALTSVSRGSSLKILSKGKRGGHSSVSTES----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             360 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31.0%; Score 568; DB 1; 35.3%; Pred. No. 4.1e-60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 69;
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                                                                     -----LKILAI----HGLISKDSLPKD
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SRPSFVGSSSGHTS

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Best Local Sim
Matches 132;
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N. PSDB; Q38747.

Rew interleukin-8 receptor aminoacid sequence - and corresp. cDNA properties of interleukin-8 receptor and gene therapy expressed in Xenopus laevis oocytes or transfected host cells, for screening ligands of IL-8 receptor and gene therapy claim 1; Fig 3; 39pp; English.

CONA libraries from 2 and 3.5 kb fractions of poly(A)+ RNA from HL60 neutrophils sepd. of a sucrose gradient were made in UniZAP. The Clibraries were screened with F3R oligonucleotide probe (from rabbit IL-8 receptor) and under low stringency with a p2 cDNA probe crown from random primers, to isolated the clone p2, encoding continuity of the p2 clone as probes. P2 may also be used to screen corrections of the p2 clone as probes. P2 may also be used to screen correctlular calcium-mobilising and ligand-binding properties.
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13-SEP-1991; US-759568.
(USSH ) US DEPT HEALTH & HUMAN SERVICE.
Murphy PM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
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Human IL-8 receptor from clone p2.
Interleukin-8 receptor; probes; gene therapy; gro receptor; intracellula-calcium mobilising; ligand-binding; MIP-2 rece
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R33420;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 117 TVNLYSSVLILAFISLDRYLAIVHATNSQRPRKLLAEKVVYVGVWIPALLLTIPDFIF--
                                                                                                                                                                                                                                                                                                                                                                                                                     229
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9 SDNYT-----EEMGSGDYDSM------KEPCFREENANFNKIFLPTIYSIIFLTGIVGN
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15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SDSFEDFWKGEDLSNYSYSSTLPPFLLDAAPC-EPESLEINKYFVVIIYALVFLLSLLGN
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                                                                                                                                                                                                                                                                              ALAFFHCCLNPILYAFLGAKFKTSAQHALTSVSRGSSLKILSKGKRGGHSSVSTES----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EVNFYSGILLLACISVDRYLAIVHATRTLTQKRYLV-KFICLSIWGLSLLLALPVLLFRR 180
                                                                                                                                                                                                                                                                                                                                                         AHMGQKHRAMRVIFAVVLIFLLCWLPYNLVLLADTLMRTQVIQETCERRNHIDRALDATE
                                                                                                                                                                                                                                                                                                                                                                                                           SKGHOKRKALKTTVILILAFFACWLPYYIGISIDSFILLEIIKQGCEFENTVHKWISITE 288
                                                                                                                                                                                                                        ILGILHSCLNPLIYAFIGQKFR---
                                                                                           SRPSFVGSSSGHTS 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            --ANVSEADDRYICDRFYPNDL--WVVVFQFQHIMVGLILPGIVILSCYCIIISKLSH 228
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Pred. No. 4e-60;
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Search completed: Job time: 28 sec

September 14, 1999,

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(HEBE/)
(KIMK/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    rheumatoid arthritis; inflammatory bounded the chronic lung inflammation; treatment; affinity purification; detection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (LEEJ/) LEE J.
Chuntharapai A, H
WPI; 95-283151/37.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R80758 standard; Protein; 360 R80758;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Interleukin 8 receptor B.
Interleukin; IL-8; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Columns 53-56; 62pp; English.

Antibodies directed against the interleukin-8 receptor B can be used to treat or prevent inflammation e.g. psoriasis, dermatitis, rheumatoid arthritis and particularly inflammatory bowel disease and chronic lung inflammation. When immobilised, these antibodies may be used to detect interleukin-8 receptor B expression in cells and tissues and for affinity purification of interleukin-8 receptor B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New antibodies against interleukin or prevent inflammation, also for o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; Q99008.
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                                                                                                                                                                                                                                                                                                                                 SDSFEDFWKGEDLSNYSYSSTLPPFLLDAAPC-EPESLEINKYFVVIIYALVFLLSLLGN
                                                                                                                                                                                                                                                                           SLYMLVILYSRYGRSYTDYYLLNLALADLLFALTLPIWAASKYNGWIFGTFLCKYVSLLK 126
                                                                                                                                                               TVYSSNVSPA-----CYEDMGNNTANWRMLLRILPQSFGFIVPLLIMLFCYGFTLRTLFK 240
                                                                                                                                                                                                                     EVNFYSGILLLACISVDRYLAIVHATRTLTQKRYLV-KFICLSIWGLSLLLALPVLLFRR
                                                                                                                                                                                                                                     TVNLVSSVLILAFISLDRYLATVHATNSQRPRKLLAEKVVYVGVWIPALLLTIPDFIF-- 175
                                                                              ALAFFHCCLNFILYAFLGAKFKTSAQHALTSVSRGSSLKILSKGKRGGHSSVSTES----
                                                                                                            AHMGQKHRAMRVIFAVVLIFLLCWLPYNLVLLADTLMRTQVIQETCERRNHIDRALDATE
                                                                                                                                    SKGHQKRKALKTTVILILAFFACWLPYYIGISIDSFILLEIIKQGCEFENTVHKWISITE
                                                                                                                                                                                        ----ANVSEADDRYICDRFYPNDL--WVVVFQFQHIMVGLILPGIVILSCYCIIISKLSH 228
SRPSFVGSSSGHTS
                                                     ILGILHSCLNPLIYAFIGQKFR---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HEBERT
                          --ESSSFHSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                           360 AA;
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; US-202056.
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   psoriasis; dermatitis;
ry bowel disease;
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4.1e-60;
ches 119;
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September 14, 1999,

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Treatment of inflammatory disorders - by administering an antibody capable of binding a platelet factor 4 superfamily receptor polypeptide

S Disclosure: Page 54-56; 83pp; English.

C PF4AR members were identified by probing lambda libraries from thuman monoclyte-like cell line HL-60 and human peripheral blood lymphocytes using a large fragment of IL-8 receptor DNA (full sequence given in Q80520). The nucleotide sequences of the 2 PF4ARs are given in Q80521 and Q80522, and their respective amino acid sequences in R68812 and R68813.

Sequence 1737 BP; 454 A; 411 C; 373 G; 499 T;
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Best Local Similarity
Matches 1737; Conserv
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22-DEC-1994.
07-JUN-1994; 1
11-JUN-1993; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18-JUL-1995 (first entry)
Human monocyte PF4AR cDNA.
Interleukin-8 receptor; IL-8 receptor; PF4AR;
Platelet factor superfamily receptor; monocyte; chemotactic;
inflammation; inflammatory disease; arthritis; emphysema; cy
fibrosis; colitis; bronchitis; meningitis; therapeutic; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chuntharapai A, H
WPI; 95-036114/05.
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11-JUN-1993; US-076093
(GETH ) GENENTECH INC.
Chuntharapai A, Hebert C,
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                      CTTCCCTTCTGGGCAGTTGATGCCGTGGCAAACTGGTACTTTGGGAACTTCCTATGCAAG
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CTTCCCTTCTGGGCAGTTGATGCCGTGGCAAACTGGTACTTTGGGAACTTCCTATGCAAG
                                                                                                           AGCATGACGGACAAGTACAGGCTGCACCTGTCAGTGGCCGACCTCCTCTTTGTCATCACG
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Human MCP-4 recept
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Sequence encoding Human IL-8 receptor

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Matches 1737; Conservative (
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or prevent inflammation, also for detecting-
purificn.

Example 2; Columns 47-50; 62pp; English.

Antibodies directed against the interleukin-8 receptor B can be
to treat or prevent inflammation e.g. psoriasis, dermatitis,
rheumatoid arthritis and particularly inflammatory bowel diseas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (KIMK/) KIM K J.
(LEEJ/) LEE J.
CHUMATHORITAI A; Hebert C
WPI; 95-283151/37.
P-PSDB; R80757.
                                                                                                                                                                                                                                              chronic lung inflammation. When immobilised, these antibodies may be used to detect interleukin-8 receptor B expression in cells and tissues and for affinity purification of interleukin-8 receptor B from cells. This sequence is an additional chemokine superfamily receptor which was identified by probing lamda libraries of genomic DNA from a human monocyte-like cell line (L-60) and human peripheral blood lymphocytes using a large fragment of the interleukin-8 type A receptor DNA (See Q99006).
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29-MAR-1991; 677211.
29-MAR-1991; US-677211.
25-FEB-1994; US-202056.
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                                                 Isolated human platelet factor 4 super-family receptor polypeptide and corresp. antibodies and DNA - useful as diagnostic and screening agents, and for treating inflammation or PF4AR-mediated disorders

Sclaim 7; Fig 4; 78pp; English.

Chaim 7; Fig 4; 78pp; English.

Screen Fire receptor cDNA sequence was isolated (see Q29505) and a contained of the coding sequence was used as a probe to screen human cell line HL60 and human peripheral blood lymphocyte CoDNA libraries. Two new gene sequences were found that are clearly crelated to the II-8 receptor. One of these was contained in combined clone 8rr.20.15 and is predicted to encode an amino acid sequence which is 34% identical with both the high and low affinity II-8 receptors. See also Q37107.

Sequence 1737 BP; 457 A; 412 C; 370 G; 498 T;
  Query Match
Best Local Similarity
                                                                                                                                                                                                                                          W09217497-A.
15-CCT-1992: U02317.
23-MAR-1991: US-677211.
29-MAR-1991: US-810782.
(GETH ) GENENTECH INC.
Holmes WE, Lee J, wood WI:
WPI: 92-756191744.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q29506 stand
Q29506;
12-MAR-1993
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New Platelet factor 4 receptor superfamily member PF

IL-8R, G-protein coupled receptor family; rhodopsin

pro-inflammatory cytokine; 8rr.20.15; ss.
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X15882; X15882; standard; cdna; 1944

X1580LT X158821 ID 882 cDNA encoding G-protein coupled receptor polypeptide designated CXCR4B.

G-protein coupled receptor; CXCR4B; human; splice variant; chemokine receptor; CXCR4; vaccine; gene therapy; HIV-1; HIV-1; cancer; pain; diabetes; obesity; anorexia; bulimia; asthma: Parkinson's disease; acute heart failure; hypotension; hypertension; urinary retention; osteoporosis; angina pectoris; myocardial infarction; stroke; ulcer; allergy; benign prostatic hypertrophy; migraine; vomiting; psychotic disorder; neurological disorder; anxiety; schizophrenia; manic depression; delirium; dementia; mental retardation; dyskinesias; Huntingtons disease; Gilles de la Tourette syndrome; ss. Homo 12-MAY-1999 CDNA encodin sapiens (first entry) Location/Qualifiers 336. .1406 /*tag= a 361

EP-897980-A2. 24-FEB-1999. 07-AUG-1998; 24-JUL-1998; 20-AUG-1997; 306324. US-056601. US-056601.

misc_feature

/*tag-/note-

b splice

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PT New 6 protein coupled receptor (CXCR4B) polypeptide and polynucleotide, human splice variant of a chemokine receptor - prolynucleotide, human splice variant of a chemokine receptor - prolynucleotide, human splice variant of a chemokine receptor prolynucleotide and for prevention and treatment of provided infection, cancer, stroke and dementia coupled receptor polypeptide CC The present sequence encodes a G-protein coupled receptor polypeptide coupled receptor CXCR4B, which is a human splice variant of a chemokine receptor CXCR4B. CXCR4B polynucleotides and polypeptides are useful for CC diagnosing susceptibility to diseases by detecting mutations or CC polymorphisms in the CXCR4B gene or analysing for integration and CC polynucleotides are also useful for screening for antagonists and CC polynucleotides are also useful for screening for antagonists and CC polynucleotides are also useful for screening for antagonists and CC polynucleotide imbalance. CXCR4B polypeptides can be administered directly (as a vaccine) or via a vector (gene therapy) to prevent disease. CC pliseases diagnosed, prevented and treated include: HIV-1 and HIV-1 CC infections; cancer; pain; diabetes; obesity; anorexia; bulimia; asthma; parkinson's disease; acute heart failure; hypotension; hypertension; cc vaniting; psychotic and neurological disorders; including anxiety, stroke; ulcers; allergies; benign prostatic hypertrophy; migraine; cc vaniting; psychotic and neurological disorders, including anxiety, schizother, and dyskinesias, such as Huntingtons disease or Gilles de CC to chromosomes, allowing gene inheritance to be studied through linkage CC analysis.
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Best Local Similarity
Matches 1579; Conserv
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1922	GATTTCAGCACCTACAGTGTACAAGTCTTGKATTAAGTTGKTAATAAAAGTACATGTTAA	1863	ф
1664	ATTTCAGCACCTACAGTGTAC-AGTCTTGTATTAAGTTGTTAATAAAAGTACATGTTA	1606	Qy
1862	TTATAACCAAAGCCCAAAGTGGTATAGAAATGCTGGTTTTTCAGTTTTCAGGAGTGGGTT	1803	DЬ
1605	TATAACCAAAGCCCAAAGTGGTATAGAAATGCTGGTTTTTCAGTTTTCAGGAGTGGGT	1546	γQ
1802	CATTCCCGTGGAACGTTTTTCCTGTTCTTAAGACGTGATTTTGCTGTAGAAGATGGCAC	1743	Db
1545	CATTCCCGTGGAACGTTTTTCCTGTTCTTAAGACGTGATTTTGCTGTAGAAGATGGCA	1486	Qу
1742	GTGTAGTGAATCACGTAAAGCTAGAAATGATCCCCAGCTGTTTATGCATAGATAATCTCT	1683	Дb
1485	TGTAGTGAATCACGTAAAAGCTAGAAATGATCCCCCAGCTGTTTATGCATAGATAATCT	1426	Qy
1682	TCTTAGTTGCTGTATGTCTCGTGGTAGGACTGTAGAAAAGGGAACTGAACATTCCAGAGC	1623	Дb
1425	CTTAGTTGCTGTATGTCTCGTGGTAGGACTGTAGAAAAGGGAACTGAACATTCCAGA	1366	Qy
1622	TTTATATAAATTTTTTTGTTTCATATTGATGTGTGTCTAGGCAGGACCTGTGGCCAAGT	1563	Дb
1365	TTATATAAATTTTTTTTTGTTTCATATTGATGTGTGTGTG	1306	Qy
1562	TATTGCTTGGAGTTTTTGTCTTGTGTGTTTTAGTTTTTGTGAAGTTTAATTGACTTA	1503	αα
1305	GCTTGTTGGATTTTTGTCTTTGTGTGTTTTTTTGTGAAGTTTAAGTTGACTT	1246	Qy
1502	ACTITITITAAGITACACAFTITTCAGATATAAAAAGACTGACCAATATTGTACAGTTTT	1443	ДĎ
1245	CTTTTTTTTAAGTTACACATTTTTCAGATATAAAAGACTGACCAATATTGTACAGTTT	1186	Qy
1442	TCTTCAAGTTTTCACTCCAGCTAACACAGATGTAAAAGACTTTTTTTT	1383	р
1185	CTTCAAGTTTTCACTCCAGCTAACACAGATGTAAAAGACTTTTTTTT	1126	Qy
1382	CTCAAGATCCTCTCCAAAGGAAAGCGAGGTGGACATTCATCTGTTTCCACTGAGTCTGAG	1323	Db
1125	TCAAGATCCTCTCCAAAGGAAAGCGAGGTGGACATTCATCTGTTTCCACTGAGTCTG	1066	Qy
1322	GAGCCAAATTTAAAACCTCTGCCCAGCACGCACTCACCTCTGTGAGCAGAGGGTCCAGC	1263	Db
1065	GAGCCAAATTTAAAAACCTCTGCCCAGCACGCACTCACCTCTGTGAGCAGAGGGTCCAG	1006	Qy
1262	ATCACCGAGGCCCTAGCTTTCTTCCACTGTTGTCTGAACCCCATCCTCTATGCTTTCCTT	1203	Дb
1005	TCACCGAGGCCCTAGCTTTCTTCCACTGTTGTCTGAACCCCATCCTCTATGCTTTCCT	946	Qy
1202	CTCCTGGAAATCATCAAGCAAGGGTGTGAGTTTGAGAACACTGTGCACAAGTGGATTTCC	1143	DЪ
945	TCCTGGAAATCATCAAGCAAGGGTGTGAGTTTGAGAACACTGTGCACAAGTGGATTTC	886	Qy
1142	CIGGCTITCTTCGCCTGTTGGCTGCCTTACTACATTGGGATCAGCATCGACTCCTTCATC	1083	Dъ
885	TGGCTTTCTTCGCCTGTTGGCTGCCTTACTACATTGGGATCAGCATCGACTCCTTCA	826	Qy
1082	CTGTCACACTCCAAGGGCCACCAGAAGCGCCAAGGCCCTCAAGACCACCATCCTCATC	1023	Дb
825	TGTCACACTCCAAGGGCCACCAGAAGCGCCAAGGCCCTCAAGACCACAGTCATCCTC	766	Qy
1022	GTTGGCCTTATCCTGCCTGGTATTGTCATCCTGTCCTGCTATTGCATTATCATCTCCAAG	963	Вb
765	TIGGCCTTATCCIGCCIGGTATIGTCATCCIGTCCIGCTATIGCATTATCATCTCCAA	706	Qy
962	TGTGACCGCTTCTACCCCAATGACTTGTGGGTGGTTGTGTTTCCAGTTTCAGCACATCATG	903	ф
705	GTGACCGCTTCTACCCCAATGACTTGTGGGTGGTTGTGTTTCCAGTTTCAGCACATCA	646	Qy

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V1835/T
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CC The present novel sequence represents the human RM3 cDNA isolated from a human macrophage cDNA library. The invention claims for the full length V28 genomic DNA sequence (V18343) isolated from a human procession contains the invention claims are seven cransmembrane (7TM) receptors which are probably involved in signal transduction. The invention also claims that cells transformed with CC v28 DNA can be used to produce the recombinant polypeptide, to produce the invention also claims that cells transformed with CC v28 DNA can be used to produce the recombinant polypeptide, to produce cantiagonists. The antibodies, agonists and antagonists or conducted the modulate v28 receptor-ligand binding, for e.g. in immunological cand/or inflammatory events in vivo.

So Sequence 1317 BP; 332 A; 342 C; 265 G; 378 T;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local
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Key

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02-JUN-1998.
17-NOV-1993;
17-NOV-1992;
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Godiska R, Gray PW, Schweickart
WPI; 98-332132/29.
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V18357;
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                                                                                                   ATCCTGGCCTTCATCAGTCTGGACCGCTACCTGGCCATCGTCCACGCCACCACCACCACTCAG
                                                                                                                                                                       AACTTCCTATGCAAGGCAGTCCATGTCATCTACAGAGTCAACCTCTACAGCAGTGTCCTC
                                                                                                                                                                                                 AACTTCCTATGCAAGGCAGTCCATGTCATCTACACAGTCAACCTCTACAGGAGTGTCCTC
                                                                                                                                                                                                                                                                        CTCTTTGTCATCACGCTTCCCCTTCTGGGCAGTTGATGCCGTGGCAAACTGGTACTTTGGG
                                                                                                                                                                                                                                                                                                     CTCTTTGTCATCACGCTTCCCTTCTGGGCAGTTGATGCCGTGGCAAACTGGTACTTTGGG
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AGGCCAAGGAAGCTGTTGGCTGAAAAGGTGGTCTATGTTGGCGTCTGGATCCCTGCCCTC
                                                                         ATCCTGGCCTTCATCAGTCTGGACCGCTACCTGGCCATCGTCCACGCCACCACACAGTCAG
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/product= "Human
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Pred. No. 8.4e-199;
0; Mismatches 3;
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                                                                                                                         09-JUN-1994.
17-NOV-1993; U11153.
17-NOV-1992; US-977452.
(ICOS-) ICOS CORP.
GODISKA R. GTAY PW, SC
WPI; 94-200264/24.
P-PSDB; R53753.
involving the receptors.
Example 11; Page 82-83; 100pp; English.
Two primers (Q66148, Q66149) were used
                                                                             DNA encoding seven trans:membrane prods for use as therapeutic or o
                                                                                                                                                                                                                                                                                                                                                                                                                              Primer; seven tra
polymerase chain
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Q66179;
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Local Similarity
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Pred. No. 1.7e-198;
0; Mismatches 4;
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Best Local Similarity
Matches 1391; Conser
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13-AUG-1998.
07-FEB-1997; W0-700299.
07-FEB-1997; W0-700299.
(SHIO ) SHIONOGI & CO LTD.
IIZASA H, KISHIMOCO T, NAGASAWA T
YOSHIda N, YOSHIE O;
WPI; 98-447332/38.
P-PSDB; W64778.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nucleic acid encoding
Mouse; CXC chemokine r
CXC chemokine pre-B ce
HIV infection; screeni
Mus sp.
Locati
CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mouse CXC chemokine receptor binding to PBSF/SDF-1 pre-B cell stimulatory factor - is useful for screening of potential HIV infection and AIDS inhibitors
Claim 3; Pages 39-42; 76pp; Japanese.
The present sequence encodes a murine CXC chemokine receptor which binds to the mouse CXC chemokine pre-B cell stimulatory factor PBSF/SDF-1. The nucleic acid is isolated from mouse pre-B cell line DW34. The receptor and cells expressing it can be used in the study and mapping of the mechanism of HIV infection and in screenin of potential inhibitors of HIV infection and the development of AII sequence 1877 BP; 469 A; 451 C; 406 G; 551 T;
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se; CXC chemokine receptor; pre-B cell line DW34;
chemokine pre-B cell stimulatory factor PBSF/SDF-1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           infection; screening; inhibitor; AIDS; ds.
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                           TTTCAATAAAATCTTCCTGCCCACCATCTACTCCATCATCTTCTTAACTGGCATTGTGGG
                                                                                                                                                                                                            GAGTGTTGCCATGGAACCGATCAGTGTGAGTATATACACTTCTGATAACTACTCTGAAGA
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                                                                                                                                                                                                                                                                CAGCGGTTACCATGGA----
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                                                TIGITGGATITTIGT-----CTIGIGITTCTTIAGITTITIGIGAAGITTAATIGACITA 1305
                                                                                            CAAAGGAAAGCGCGGTGGACACTCTTCCGTCTCCACGGAGTCAGAATCCTCCAGTTTTCA
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PN EP-897980 PD 24-FEB-199 PF 07-AUG-199 PR 20-AUG-199 PR 20-AUG-199 PR (SMIK) SN PI Gupta SK, DR WPI; 99-11 DR P-PSDB; WP PT New G proto PT useful as PT HIV infect PS Claim 13; CC The present CC designates CC diagnosing CC of CXCR4B CC of CXCR4B CC polymucle	RESULT 8 RESULT 8 X15883 Sta X158	582 730 TT 624 GT 790 GT	Oy 1489 Db 1610 TGTTTG OY 1526 TTTGCT Db 1670 TTTTCT	1490 ACA 1474 TAG 1 1550 TAA	Db 1370 ATATA Oy 1362 AAGTT
N EP-897980-A2. D 24-FEB-1999: D 7-AUG-1998: 306324. F 77-AUG-1998: US-056601. R 20-AUG-1998: US-056601. R 20-AUG-1998: US-056601. A (SMIK) SMITHKLINE BEECHAM CORP. A (SMIK) SMITHKLINE BEECHAM CORP. I Gupta SK, Pillarisetti K; I Gupta SK, Pillarisetti K; R WPI; 99-134643/12. R WPI; 99-134643/12. T New G protein coupled receptor (CXCR4B) polypeptide and polynucleotide, human splice variant of a chemokine receptor useful as diagnostic reagents and for prevention and treatment of T Useful as diagnostic reagents and dementia T HIV infection, cancer, stroke and dementia Claim 13; Page 18; 24pp; English. C The present sequence encodes a partial G-protein coupled receptor Cdesignated CXCR4B, which is a human splice variant of a chemokine creceptor CXCR4. CXCR4B polynucleotides and polypeptides are useful c diagnosing susceptibility to diseases by detecting mutations or c polymorphisms in the CXCR4B gene or analysing for the presence or polymorphisms in the CXCR4B gene or analysing for antagonists and collectides are also useful for screening for antagonists and	AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	TCA TCA AAG AAG	TITTCCTGTAAAAAGACGTGAT TITTTCCTGTTATGACGACGTGAT TITTTGCTTATGCTGTGTGTATGTTTTTTTTTTTTTTTTT		AAATATIGTTTTTGTTTGTTTTCATGTGAATGAGCGTCTAGGCAGGACCTGTGCC TCTTAGTTGCTATGTCTCGTGGTAGGACTGTAGAAAAGGGAACTG
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Best Local Similarity
Matches 249; Conserv
Claim 1; page 571-572; 2245pp; Japanese. A single-stranded DNA (or its complementary strand or the corresp. double-stranded DNA) which comprises one of the 7837 "GS" sequences given in Tig001-Tig0837 and which is able to hybridise to part of human genomic DNA, CDNA or mRNA is claimed. The GS (Gene Signature) sequences were obtained from 3'-directed CDNA libraries prepared from various human tissues; synthesis of CDNA was initiated from the 3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-untranslated sequence is unique to a particular mRNA species, almost
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            agonists which can be used to treat conditions associated with CXCR4B polypeptide imbalance. CXCR4B polypeptides can be administered directly (as a vaccine) or via a vector (gene therapy) to prevent disease. Diseases diagnosed, prevented and treated include: HIV-1 and HIV-1 infections; cancer; pain; diabetes; obesity; anorexia; bulimia; asthma; Parkinson's disease; acute heart failure; hypotension; hypertension; urinary retention; osteoporosis; angina pectoris; myocardial infarction; stroke; ulcers; allergies; benign prostatic hypertrophy; migraine; vomiting; psychotic and neurological disorders, including anxiety, schizophrenia, manic depression, delirium, dementia and severe mental retardation; and dyskinesias, such as Huntingtons disease or Gilles de la Tourette syndrome. CXCR4B polypeptides are useful for mapping genes analysis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gene signature; messenger RNA; mRNA; relative abundance; frequency; human; cloning; mapping; non-biased library; diagnosis; detection; cell typing; abnormal cell function; ss.
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11-NOV-1994; J01916.
12-NOV-1993; JP-355504
                                                                                                                                                                                                                                                                                                                                                                                                  Identifying gene signatures in 3'-directed human cDNA library -
for diagnosis of abnormal cell function, by preparing cDNA that
reflects relative abundance of corresp. mRNA in specific human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matsubara K, Okubo K; WPI; 95-206931/27.
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               interleukin-8 binding antagonists, used to treat inflammation

bisclosure; Fig 1; 71pp; Engilsh.

Rabbit high affinity IL-8 receptor gene was isolated from rabbit peritoneal neutrophils and used as a source of poly(A) + RNA, to produce a rabbit neutrophil cDNA library. 250,000 recombinant plaques were screened for those which hybridized to an antisense oligonucleotide (030015). This probe was designed based on the sequence derived from the second transmembrane domain of G-protein-coupled receptors. After tertiary screening, six plaques were isolated. The insert of one of these plaques, termed F3R was of 2.5 kb in size. This insert was sequenced. The protein deduced from the F3R clone demonstrates that it belongs to the family of G-protein-coupled receptors. The deduced protein sequence indicates seven putatuve transmembrane segments.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local S
Matches 218
                                                                                                                                                                                                                                                                                                                                                                                             29-OCT-1992.
10-APR-1992; U02977.
10-APR-1991; US-685101.
09-JUL-1991; US-726606.
09-DEC-1991; US-803842.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence encoding a high affinity recombinant rabbit in (IL-8) receptor polypeptide in F3R.
IL-8 receptor polypeptide; G-protein-coupled receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           all the 3'-oriented cDNAs hybridise with specific mRNAs. Each library is constructed so as to reflect accurately the relative abundance of different mRNAs in the particular tissue from which it was derived. The appearance frequency of a given GS in a cDNA library can be determined (esp. using primers and probes derived from the GS sequences) as a means of diagnosing abnormal cell function or for recognising different cell types.

Sequence 218 BP; 61 A; 38 C; 44 G; 75 T;
                                                                                                                                                                                                                                                                                                                      (REPK) REPLIGEN CORP.
(UYBO-) UNIV BOSTON.
Navarro J, Thomas KM, WPI; 92-382123/46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Oryctolagus cuniculus
Key Locat
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                                                                                                                                                                                                                                                               Recombinant mammalian interleukin-8 receptor - used for screening interleukin-8 binding antagonists, used to treat inflammation
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putatuve transmembrane segments.
BP; 234 A; 366 C; 294 G
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Best Local Similarity

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Oryctolagus
Key
cds
                                                              Recombinant high affinity interleukin-8 receptor subtype A encoding I1-8A; IL-8B; receptor; monoclonal antibody; inflammatory disorder; anaphylaxis; systemic lupus erythematosus; rheumatoid arthritis; systemic necrotising vasculitis; psoriasis; asthma; allergy; ARDS; adult respiratory distress syndrome; neutrophil detection; ss.
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24-APR-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 CGTGTCAGCGTCGCAATGACATTGACCGGGCCCTGGACGCCACCGAGATTCTGGGCTTCC
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                                             cuniculus
                                                                                                                                                                                   (first entry)
                   Location/Qualifiers
                                                                                                                                                                                                                                   ВP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TATATCTGTGACCGCTTCTACCCCCAATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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y useful for treating inflammatory disorders, for detecting resembling Inflammatory disorders, for detecting resembling III-8 receptor from liq.mixt.

The neutrophil(s) and for isolating IL-8 receptor from liq.mixt.

Scalaim 2; Fig lA-B; 74pp; English.

Monoclonal antibodies were raised against recombinant interleukin-8 (II-8) receptor subtypes A and B from both human and rabbit sources (R80950-53 encoded by Q99949-52). The A subtype receptor (II-8rA) is a low affinity receptor and the B subtype receptor (II-8rB) is a low affinity receptor. The monoclonal antibody (mAb) pref. binds to the II-8 binding domain thus blocking its activation. The mabs are useful for treating inflammatory disorders (see key words) and for detecting the presence of neutrophils in a biological sample. The mAbs are also useful in the isolation of II-8 receptors from a mixture.

Sequence 1200 BP; 234 A; 366 C; 295 G; 303 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local S
Matches 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      W09525126-A1.
21-SEP -1995.
09-MAR-1995; U03032.
15-MAR-1994; US-210250.
02-MAY-1994; US-237937.
(REPK ) REPLICEN CORP.
(UYBO-) UNIV BOSTON.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Greenfield Witt DT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P-PSDB;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  95-336945/43.
                     TGGTCATGCTGTTTTGCTATGGGTTCACCCTGCGCACGCTGTTCCAGGCCCACATGGGGC
                                                                   TTGTCATCCTGCTGCTATTGCATTATCATCTCCAAGCTGTCACACTCCAAGGGCCACC
                                                                                                                                                                                                                                                                                                                               TCTATGTTGGCGTCTGGATCCCTGCCTGCCTGACTATTCCCGACTTCATCTTTGCCA 616
                                                                                                                                                                                                                                                                                                                                                                                                                                            TGGCCATCGTCCACGCCACCAACAGTCAGAGGCCCAAGGAAGCTGTTGGCTGAAAAAGGTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TTGATGCCGTGGCAAACTGGTACTTTGGGAACTTCCTATGCAAGGCAGTCCATGTCATCT 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACTCCCTGGTGATGCTGGTCATACTGTACAGCCGGAGCAACCGTTCGGTCACCGACGTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       THAACAAATATGTTGTGGTCGTCATCTATGCCCTGGTCTTCCTGCTGAGCCTGCTGGGCA 291
                                                                                                                                                                                                             AAGTCTTTTCTCCAAACAATTCCAGCCCGGTCTGCTATGAGGACCTGGGTCACAACACAG
                                                                                                                                                                                                                                                         ACGTCAGTGAGGCAGATGACAGA-----
                                                                                                                                                                                                                                                                                                       TATGTCTGGGCATCTGGGCGCTGTCTCTGATTTTGTCCCTGCCCTTCTTCCTCTTCCGCC
                                                                                                                                                                                                                                                                                                                                                                                                   TGGCCATTGTCCATGCTACTCGCACACTGACCCCAGAAGCGCCACTTG---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AGGAAGTCAACTTCTACAGTGGAATCCTGCTCCTGGCCTGCATCAGTGTGGACCGCTACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACACAGTCAACCTCTACAGCAGTGTCCTCATCCTGGCCTTCATCAGTCTGGACCGCTACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TCTCCAAGGAAAAAGGCTGGATTTTCGGCACGCCCCTGTGCAAGGTGGTCTCGCTTGTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACCTGCTGAACCTGGCCATGGCCGACCTGCTTTTTGCCCTGACCATGCCTATCTGGGCCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Larosa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 206.8; DB 1;
Pred. No. 4.1e-30;
0; Mismatches 362;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Navarro
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Length

mixture

12;

Gaps

2

-GTCAAGTTCA

667

648

787 768 727 496 471

531

411

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                                                                                                                                                                                                                                                       Monoclonal antibody against recombinant IL-8 receptor polypeptide - y useful for treating inflammatory disorders, for detecting reutrophil(s) and for isolating IL-8 receptor from liq.mixt.

Claim 6; Fig 3A-B; 74pp; English.

Monoclonal antibodies were raised against recombinant interleukin-8 (IL-8) receptor subtypes A and B from both human and rabbit sources (R80950-53 encoded by 099949-52). The A subtype receptor (IL-8rA) is a low affinity receptor and the B subtype receptor (IL-8rB) is a low affinity receptor. The monoclonal antibody (mab) pref. binds to the IL-8 binding domain thus blocking its activation. The mabs are useful for treating inflammatory disorders (see key words) and for detecting the presence of neutrophils in a biological sample. The mabs are also useful in the isolation of IL-8 receptors from a mixture.

Sequence 1373 BP; 266 A; 437 C; 329 G; 335 T;
                                                                                                                                                                              Query Match
Best Local S
Matches 467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO9525126-A1.
21-SEP-1995.
09-MAR-1995; U03032.
15-MAR-1994; US-210250.
02-MAY-1994; US-237937.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24-APR-1996 (first entry)
Recombinant high affinity interleukin-8 receptor subtype B encoding Il-8A; IL-8B; receptor; monoclonal antibody; inflammatory disorder; anaphylaxis; systemic lupus erythematosus; rheumatoid arthritis; systemic necrotising vasculitis; psoriasis; asthma; allergy; ARDS; systemic necrotising vasculitis; psoriasis; asthma; allergy; ARDS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q99951;
24-APR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Oryctolagus cuniculus.
Key Locati
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Greenfield EA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   099951
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P-PSDB; R80952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (REPK ) REPLIGEN CORP. (UYBO-) UNIV BOSTON.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1009
                    295
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CTGAGAAGCATGACGGACAAGTACAGGCTGCACCTGTCAGTGGCCGACCTCCTTTTGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        95-336945/43.
                                                 TTCCTGCTGAGCCTGCTGGGCAACTCCCTGGTGATGCTGGTCATCCTGTACAGCCGGAGC
                                                                               TTCTTAACTGGCATTGTGGGCAATGGATTGGTCATCCTGGTCATGGGTTACCAGAAGAAA
                                                                                                              TGCCGGTCAGAATCTCTGGAAACCAACAGCTATGTTGTGCTCATCACCTATATCCTGGTC
                                                                                                                                           TTCCGTGAAGAAAATGCTAATTTCAATAAAATCTTCCTGCCCACCATCTACTCCATCATC 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TGCACAGCTGCCTCAACCCCCATCATCTACGCCTTCATTGGCCAAAACTTT 1058
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TCCACTGTTGTCTGAACCCCCATCCTATGCTTTCCTTTGGAGCCAAATTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CGTGTCAGCGTCGCAATGACATTGACCGGGCCCTGGACGCCACCGAGATTCTGGGCTTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGTGTGAGTTTGAGAACACTGTGCACAAGTGGATTTCCATCACCGAGGCCCTAGCTTTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TGCCCTACAACCTGGTCCTGCTCGCAGACACCCTCATGAGGACCCACGTGATCCAGGAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AGAAGCGCAAGGCCCTCAAGACCACAGTCATCCTCATCCTGGCTTTCTTCGCCTGTTGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            respiratory distress syndrome;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   standard;
                                                                                                                                                                                             Similarity
                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Larosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA; 1373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                             11.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ВP
                                                                                                                                                                            0;
                                                                                                                                                                                          Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Navarro
                                                                                                                                                                                Mismatches
                                                                                                                                                                           e 201.2; DB 1;
No. 4.6e-29;
ismatches 373;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ŗ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  neutrophil detection;
                                                                                                                                                                              Indels
                                                                                                                                                                                                        Length
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                                                                                                                                                                                                             1373;
                                                                                                                                                                            12;
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                                                                                                                                                                            Gaps
                                                 298
                                                                               294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1008
                354
                                                                                                               238
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15-0CT-1992; U02317.
23-MAR-1992; U02317.
29-MAR-1991; US-677211.
19-DEC-1991; US-810782.
(GETH ) GENENTECH INC.
HOlmes WE, Lee J, Wood WPI: 92-366191/44.
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Q29505;
12-MAR-1993
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                                                                                                                                          Location/Qualifiers 51. .1103
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Best Local Similarity Matches 455; Conserv
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Best Local
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A cDNA library constructed from human neutrophil mRNA in the mammali expression vector pRK5B was transfected into COS-7 cells as pools of 2500 clones. One positive pool from the first 58 transfections was partitioned into smaller pools until a pure clone (pRK5B.il8r1.1) was obtained. The ORF encodes a protein of 350 amino acids which shares several features with the G-protein coupled receptors of the rhodopsin superfamily, including 7 hydrophobic (transmembrane) domains. See also 029506 and 037107.
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                                          GGTGATCCAGGAGACCTGTGAGCACCGCAACAACATCGGCCGGGCCCTGGATGCCACTGA
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GGCCCTAGCTTTCTTCCACTGTTGTCTGAACCCCATCCTCTATGCTTTCCTTGGAGCCAA
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Pred. No. 3.2e-28;
0; Mismatches 377
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Best Local
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A cDNA library constructed from human neutrophil mRNA in pRK5B was transfected into COS-7 cells, and the cells were screened with 1251 IL-8. The DNA sequence of isolated cDNA clone pRK5B.il8r1.1, encoding human IL-8 receptor, is given in Q80520 and the predicted amino acid sequence in R68811. The receptor is used to raise antibodies that neutralize the activity of pF4AR, e.g. IL-8 recepto Sequence 1933 BP; 422 A; 540 C; 485 G; 486 T:
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07-JUN-1994;
11-JUN-1993;
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Interleukin-8 receptor; IL-8 receptor; PF4AR;
Platelet factor superfamily receptor; neutrophil; chemotactic;
platelet factor superfamily receptor; arthritis; emphysema; cyst
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P-PSDB; R68811
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11-JUN-1993; US-076093.
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                                                                                                                                                              (HEBE/) HEBERT C.

(KIMK/) KIM K J.

(LEEJ/) LEE J.

Chuntharapai A. Hebert C. Kim KJ. Lee J.

WPI: 95-283151/37.

P-PSDB: R80756.

New antibodies against interleukin 8 type B re
or prevent inflammation, also for detecting re
purificen.

Example 2: Columns 43-46; 62pp; English.
                                                                                                                                                                                                                                                                                                                 08-AUG-1995.
29-MAR-1991; 677211.
29-MAR-1991; US-677211.
29-MAR-1991; US-677211.
25-FEB-1994; US-202056.
type B re
Sequence
                         Example 2; Columns 43-46; 62pp; English.
Antibodies directed against the interleukin-8 receptor B can be u
to treat or prevent inflammation e.g. psoriasis, dermatitis,
rheumatoid arthritis and particularly inflammatory bowel disease
chronic lung inflammation. When immobilised, these antibodies ma
be used to detect interleukin-8 receptor B expression in cells and
tissues and for affinity purification of interleukin-8 receptor B
from cells. A sequence obtained from this CDNA insert, which
encodes the high affinity interleukin-8 receptor, was used to
probe lambda gt10 cDNA libraries for the human interleukin-8
                                                                                                                                                                                                                                                                                                                                                                                                                       Interleukin: IL-8; inflammation; psoriasis; derma rheumatoid arthritis; inflammatory bowel disease; chronic lung inflammation; treatment; antibody; affinity purification; detection; ss.
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(HEBE/) HEBERT C.
(KIMK/) KIM K J.
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Interleukin 8 receptor A c
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	G28514 human STS 52514 human (clon AF005572 Homo sapien AJ009816 Felis Cat L01639 Human (clon AF019378 Cercopith U89798 Pan troylod AF025375 Homo sapien AF019378 Cercoeb JAF019378 Chloroceb JAF019374 Macaca mula AF051943 Chloroceb U93311 Macaca mula JAF051940 Cercoebu M86739 Cow neurope D8774 Mus musculus M86739 Cow neurope D8774 Mus musculus X99582 M.musculus X99581 M.musculus X99581 M.musculus X99581 M.musculus Z80113 Mus musculu Z80113 Mus musculu Z80113 Mus musculu U54791 Rattus norv Y17894 Xenopus lae U17894 Xenopus lae U3942 Ovis artles AJ0012310 Cyprinus Z80111 Mus musculu W74240 Oryctolagus M82873 Oryctolagus	I13753 Sequence 4 I24455 Sequence 3

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DEFINITION
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VERSION
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KEYWORDS
SOURCE
Unknown.
ORGANISM
Unknown.
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AUTHORS
Lee, J. and Wood, W.I.
TITLE
FARTLES
LOCATION/Qualifiers
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1 GAATTCCAGTGTGCTGGCGGCGCGGCGCAAAGTGACGCCGAGGGCCTGAGTGCTCCAGT	ery Match 100.0%; Score 1737; DB 5; Length 1737; st Local Similarity 100.0%; Pred. No. 0; tches 1737; Conservative 0; Mismatches 0; Indels 0;	URCE Unknown. ORGANISM Unknown. Unclassified. Unclassifi	. 19181	681 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	621 P		1501 GTITTTCCTGTICTTAAGACGTGATTTTGCTGTAGAAGATGGCACTTATAACCAAAGCC	1441 TAAAGCTAGAAATGATCCCCAGCTGTTTATGCATAGATAATCTCTCCATTCCCGTGGAAC	1381 GTCTCGTGGTAGGACTGTAGAAAAGGGAACTGAACATTCCAGAGCGTGTAGTGAATCACG	1321 TITGTTTCATATTGATGTGTGTCTAGGCAGGACCTGTGGCCAAGTTCTTAGTTGCTGTAT	1261 TITTGICTTGIGTTTCTITAGTITTITGTGAAGTTTAATTGACTTAITTATATAAATITT 	1201 ACACATTITICAGATATAAAAGACTGACCAATATTGTACAGTTTTTATTGCTTGTGGAT	1141 TCCAGCTAACACAGATGTAAAAGACTTTTTTTATACGATAAATAA	081 AAAGGAAAGCGAGGTGGACATTCATCTGTTTCCACTGAGTCTGAGTCTTCAAGTTTTC
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                                                                           Kanazawa,
Japan
Phone: 07
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D10924.1
                                                                                                                                                                          Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1664)

Nomura,H., Nielsen,B.W. and Matsushima,K.

Molecular cloning of cDNAs encoding a LD7

leukocyte chemotactic peptide receptors

Int. Immunol. 5 (10), 1239-1249 (1993)
                                                                                                                                Hideki Nomura
Dept. of Pharmacol.
                                                                                                                                                                                                                                                       Homo sapiens monocyte, Homo sapiens
                                                                                                                                                                                                                                                                 GTP-binding protein; plasma membrane protein; Homo sapiens monocyte, cDNA to mRNA.
                                                                                                            Cancer Res. Inst.,
13-1 Takaramachi
                                                                                                                                                       Submitted (13-Apr-1992)
                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Vertebrata;
                                                                                                                                                                                                                                                                                                                        mRNA
                                                                 0762-62-8151
0762-60-7704
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                                                      Location/Qualifiers
                                                                                                  Ishikawa
                                                                                                                                                                                                                                                                                       GI:219868
                                                                                                                                                                                                                                                                                                                      1664 bp
                                                                                                                      Kanazawa
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AACGTCAGTGAGGCAGATGACAGATATATCTGTGACCGCTTCTACCCCAATGACTTGTGG
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                                                       AACGTCAGTGAGGCAGATGACAGATATATCTGTGACCGCTTCTACCCCAATGACTTGTGG
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WIPALLLTIDDFIFANVSEADDRYICDRFYENDLWVVVFOFOHINYGLILDGIVILSC
YCIIISKLSHSKGHOKRKALKTTVILLILAFFACMILPYYIGISIDSFILLEIIKQGCEF
ENTVHKWISITEALAFFHCCLNDILYAFIGAKFKTSAQHALTSVSRGSSLKILSKGKR
GGHSSYSTESESSSFHSS"
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77. .1135
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Pred. No. 5.6e-290;
0; Mismatches 6;
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RESULT 5
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VERSION

1664 bp human STS SHGC-31461, (G28514 G28514.1 G1:1408329 G28514.1 G1:1408329 STS; STS sequence: prim.

DNA sequence

tagged

SITS.

01-JUL-1996

KEYWORDS

sequence; primer; sequence tagged site

	2 ATTAAGTTGTTAATAAAAGTACATGTTAAACTTAAAAA	162	D
	6 ATTAAGTTGTTAATAAAAAGTACATGTTAAAACTTAAAAAAAA	163	Qy
1621		156	D.
1635	6 IGCTGGTTTTTCAGTTTTCAGGAGTGGGTTGATTTCAGCACCTACAGTGTACAGTCTTG	157	γo
1561	2 AAGACGTGATTTTGCTGTAGAAGATGGCACTTATAACCAAAGCCCAAAGTGGTATAGAAA	150	밁
1575	6 AAGACGTGATTTTGCTGTAGAAGATGGCACTTATAACCAAAGCCCCAAAGTGGTATAGAAA	151	οy
1501	2 TCCCCAGCTGTTTATGCATAGATATCTCTCCATTCCCGTGGAACGTTTTTCCTGTTCTT	144	뮻
1515	6 TCCCCAGCTGTTTATGCATAGATAATCTCTCCATTCCCGTGGAACGTTTTTTCCTGTTCTT	145	VΩ
1441	2 TGTAGAAAAGGGAACTGAACATTCCAGAGCGTGTAGTTAATCACGTAAAGCTAGAAATGA	138	뮍
1455	6 TGTAGAAAAGGGAACTGAAACATTCCAGAGCGTGAAGTGAAATGACTAGAAATGA	139	γΩ
1381	2 TGTGTGTCTAGGCAGGACCTGTGGCCCAAGTTCTTAGTTGCTGTATGTCTCGTGGTAGGAC	132	Д
1395	6 TGTGTGTCTAGGCAGGACCTGTGGCCAAGTICTTAGTTGCTGTATGTCTCGTGGTAGGAC	133	Qy
1321		126	Db
1335	6 CITTAGTITITGTGAAGTTTAATTGACTTATTTATATAAATTTTTTTTTT	127	δ
1261	2 ATAAAAGACTGACCAATATTGTACAGTTTTTATTGCTTGGTTGG	120	Д
1275	6 ATAAAAGACTGACCAATATTGTACAGTTTTTATTGCTTGTTGGGATTTTTTGTCTTGTGTTT	121	γQ
1201	2 TGTAAAAGACTTTTTTTATACGATAAATAACTTTTTTTAAGTTACACATTTTTCAGAT	_	망
1215	6 TGTAAAAGACTTTTTTTTATACGATAAATAACTTTTTTTT	. 115	γo
1141	32 GGACATTCATCTGTTTCCACTGAGTCTGAGTCTTCAAGTTTTCACTCCAGCTAACACAGA	108	Дb
1155	6 GGACATTCATCTGTTTCCACTGAGTCTGAGTCTTCAAGTTTTTCACTCCAGCTAACACAG	, 109	φ
1081	22 GCACTCACCTCTGTGAGCAGAGGGTCCAGCCTCAAGATCCTCTCCAAAGGAAAGCGAGGT	102	Дb
1095	6 GCACTCACCTCTGTGAGCAGAGGGTCCAGCCTCAAGATCCTCTCCAAAGGAAAGCGAGG	103	δÕ
1021	52 TGTCTGAACCCCATCCTCTATGCTTTCCTTGGAGCCAAATTTAAAACCTCTGCCCAGCAC) 96	D
1035	6 TGTCTGAACCCCATCCTCTATGCTTTCCTTGGAGCCAAATTTAAAACCTCTGCCCAGCA	, 97	Qγ
961	02 TTTGAGAACACTGTGCACAAGTGGATTTCCATCACCGAGGCCCTAGCTTTCTTCCACTGT	90	Db
975	6 TTTGAGAACACTGTGCACAAGTGGATTTCCATCACCGAGGCCCTAGCTTTCTTCCACTG	, 91	Qy
901	2 TACATT	84	밁
915	6 TACATIGGGATCAGCATCGACTCCTTCATCCTCCTGGAAATCATCAAGCAAG	, 85	γΩ
841	32 AAGGCCCTCAAGACCACAGTCATCCTCATCCTTGCTTTCGCCTGTTTGGCTTGCCTTAC	78	망
855	6 AAGGCCCTCAAGACCACAGTCATCCTCATCCTGGCTTTCTTCGCCTGTTGGCTGCCTTA	, 79	γQ
781	22 CTGTCCTGCTATTGCATTATCATCTCCAAGCTGTCACACTCCAAGGGCCACCAGAAGCGC	72	맖
795	6 CTGTCCTGCTATTGCATTATCATCTCCAAGCTGTCACACTCCAAGGGCCACCAGAAGCG	, 73	δõ

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ORGANISM
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Best Local Similarity
Matches 1657; Conserv
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 182
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                                                                                                                   GGCGGGGGGGGAAAGTGACGCCGAGGGCCTGAGTGCTCCAGTAGCCACCGCATCTGGA 75
                                                                                       GAACCAGCGGTTACCATGGAGGGGATCAGTATATACACTTCAGATAACTACACCGAGGAA 135
                                                ATGGGCTCAGGGGACTATGACTCCATGAAGGAACCCTGTTTCCGTGAAGAAAATGCTAAT 195
                                                                             GAACCAGCGGTTACCATGGAGGGGATCAGTATATACACTTCAGATAACTACACCGAGGAA
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TTCAATAAAATCTTCCTGCCCACCATCTACTCCATCATCTTTAACTGGCATTGTGGGC
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                                                                                                                                                                                                                                                                                                Prepared with primer pairs provided by Sandoz, derived -- Washington University/Merck EST sequence.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Primer A: TIGTACAGTITTTATTGCTTGG
Primer B: CGTGATTAACTACACGCTCTGG
STS size: 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Stanford Human Genome Center (SHGC)
Stanford University School of Medicine
Department of Genetics, M-344, Stanford,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.

[ (bases 1 to 1664)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Myers,R.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: myers@shgc.stanford.
                                                                                                                                                                                                                      414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Profile:
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: 4157259689
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                                                                                                                                                            Conservative
                                                                                                                                                                                                                                       /organism="Homo sapiens"
/db_xref="taxon:9606"
/map="2"
1220. .1426
1220. .1244
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                                                                                                                                                                                                                                                                                                                                                  MgCl2:
KCl:
Tris-HCl:
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Polymerization:
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Pred. No. 5.6e-290;
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Primates; Catarrhini; Hominidae;
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G protein-coupled receptor; neuropeptide receptor.
Human adult lung cDNA to mRNA.
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Eutheria: Primates: Catarrhini: Hominidae: Homo.
1 (bases 1 to 1670)
Herzog, H., Hort, Y.J., Shine, J. and Selbie, L.A.
Molecular cloning, characterization, and localization
                                                                   homolog to the reported bovine NP and activation DNA Cell Biol. 12, 465-471 (1993)
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                /organism="Homo sapiens"
/db_xref="taxon:9606"
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/tissue_type="lung"
         /dev_stage="adult"
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Institute of Research, 13 Taft Court,
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                                                                                                                  h 90.0%; Score 1564; DB 11; Similarity 100.0%; Pred. No. 7.8e-274; 64; Conservative 0; Mismatches 0;
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Wegner, S.A., Ehrenberg, P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished
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/protein_id="AAB33982.1"
/protein_id="AAB33982.1"
/db_xref="pl0:92735719"
/db_xref="GI:2735719"
/db_xref="GI:2735719"
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YFGNFLCKAVHVITYVNLYSSVLILAFISLDRYLAIVHATNSQRPRKLLAEXVVYVGV
WIPALLLTIPDFIFANVSEADDRYICDRFYPNDLWVVFQFQFHLMVGLTLPGTVILSC
YCIISKLSHSKGHOKRALKTTVLLLLAFFACHLPYYIGISIDSFILLEIIKOGCER
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/gene="CXCR-4"
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the syncytium-inducing phenotype"
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/product="chemokine receptor"
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Homo sapiens
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                                                                                                              /clone_lib="24D3"
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CTCTTTGTCATCACGCTTCCCTTCTGGGCAGTTGATGCCGTGGCAAACTGGTACTTTGGG
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Direct Submission
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Caruz, A., Samsom, M., Alonso, J.M., Alcami, J., Baleux, F., Virelizier, J.L., Parmentier, M. and Arenzana-Seisdedos, F. Genomic organization and promoter characterization of human
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1 (bases 1 to 1637)
Federsppiel, B., Melhado, I.G., Duncan, A.M., Delaney, A., Schappert, K., Clark-Lewis, I. and Jirik, F.R.
Molecular cloning of the cDNA and chromosomal localization of the gene for a putative seven-transmembrane segment (7-TMS) receptor isolated from human spleen Genomics 16, 707-712 (1993)
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M99293.1 GI:292516
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YSIIFLIGIVONGLVILVMGYOKKLRSWTDKYRLLLSVADLLENTTLPFWAVDAVANW
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WIPALLLTIPDEIFANVSEADDRYICDRFYPNDLWVVVFQFGHIMVGLILEIIKQGCEF
YCIIISKLSHSKGHQKRKALKITVILILAFFACWLPYYIGISIDSFILLEIIKQGCEF
ENTUKMISITEALAFFHCCLNPILYAFLGAKFKTSAQHALTSVSRGSSLKILSKGKR
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399 c 363 g
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/product="seven transmembrane
/protein_id="AAA16617.1"
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/db_xref="GI:292517"
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                                                                                                         Direct Submission
Submitted (03-SEP-1997)
Toxicology, Albert-Einst
                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia;
Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 3733)
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/gene="CXCR4"
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                                                             /organism="Homo sapiens"
/db_xref="taxon:9606"
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                 GTTGGCCTTATCCTGCCTGGTATTGTCATCCTGTCCTGCTATTGCATTATCATCTCCAAG 765
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ENTVHKWISITEALAFFECCLNPILYAFLGAKFKTSAQHALTSVSRGSSLKILSKGKR
GGHSSVSTESESSSFHSS"
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/protein_id="CAA75034.1/
/db_xref="PID:e1285584"
/db_xref="PID:g3021394"
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TGTGGCAAACTGGTATTTTGGAAAGTTTCTGTGCAAGGCAGTCCATGTCATCTACACAGT
                     CGTGGCAAACTGGTACTTTGGGAACTTCCTATGCAAGGCAGTCCATGTCATCTACACAGT
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                                                                                              GCACCTATCTGTGGCAGACCTCCTCTTGTCCTCACACTTCCCTTCTGGGCAGTTGATGC
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KovacS,E.M., Baxter,G.D. and Robinson,W.F.

Feline peripheral blood mononuclear cells

CXC and CC type chemokines

Arch. Virol. 144, 273-285 (1999)
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/protein_id="CAO8839.1"
/protein_id="CAO8839.1"
/db_xref="piD:e1373135"
/db_xref="piD:e1373135"
/db_xref="piD:e1373135"
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/db_xref="piD:e137
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/cell_type-"peripheral blood mod
/dev_stage-"adult"
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/db_xref="taxon:9685"
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1 (bases 1 to 1225)

1 azin,E.E., Yoo,H., Blomqvist,A.G., Yee,F., Weng,G., Walker, Salon,J., Larhammar,D. and Wahlestedt,C.

A proposed bovine neuropeptide Y (NPY) receptor cDNA clone, human homologue, confers neither NPY binding sites nor NPY responsiveness on transfected cells

responsiveness on transfected cells

responsiveness on transfected cells
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SOURCE
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Holtkamp,N., Baier,M. and
Direct Submission
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Cercopithecus
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Paul-Ehrlich-Str.51-59,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished
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ENTVHKWISITEALAFFHCCLMPILYAFLGAKFKTSAQHALTSVSRGSSLKILSKGKR
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294 t
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Langen 63225, Germany
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(CXCR4) mRN
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	TGTTTCCACTGAGTCTGAGTCTTCAAGTTTTCACTCCAGCTAA 1126	1084	Дb
	- വ	1107	Qy
1083		1024	дb
1106	GTGAGCAGAGGGTCCAGCCTCAAGATCCTCTCCAAAGGAAAGCGAGGTGGACATTCA	1047	Qy
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1046	CATCCTCTATGCTTTCCTTGGAGCCAAATTTAAAACCTCTGCCCAGCACGCAC	987	Qy
963	TGTGCACAAGTGGATTTCCATCACCGAGGCCCTAGCTTTTTTCCACTGTTGTCTGAACCC	904	DЪ
986	- ດ	927	Qy
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926	CAGCATCGACCTCCTTCATCCTCCTGGAAATCATCAAGCAAG	867	Qy
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783	TTGCATTATCATCTCCAAGCTGTCACACTCCAAGGGCCAGCAGAAGGGCCAGAAGGCCCTCAA	724	DЪ
806	TTGCATTATCATCTCCAAGCTGTCACACTCCAAGGGCCACCAGAAGGCCCAAGGCCCTCAA	747	Qy
723	CAGTTTCAGCATCATGGTTGGCCTATCCTGCCTGGTATTGTCATCCTGCCTG	664	DЪ
746	CCAGTTTCAGCACATCATGGTTGGCCTTATCCTGCTGGTATTGTCCTGCTCTGCTA	687	Qγ
663	GGCAGATGACAGATATCTGTGACCGCTTCTACCCCAATGACTTGTGGGTGG	604	Db
686	GCAGATGACAGATATATCTGTGACCGCTTCTACCCCAATGACTTGTGGGTGG	627	Qy
603	TGTCTGGATCCCTGCCTGCCTGACTATTCCCGACTTCATCTTTGCCAGCGTCAGTGA	544	Вb
626	CGTCAGTGA	567	Qγ
543	CACGCCACCAACAGTCAGAAGCCAAGGAAGCTGTTGGCTGAAAAGGTGGTCTATGTTGG	484	DЪ
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483	CCTCTACAGCAGTGTCCTCATCCTGGCCTTCATCAGTCTGGACCGCTACCTGGCCATTGT	424	DЪ
506	CTCTACAGCAGTGTCCTCATCCTGGCCTTCATCAGTCTGGACCGCTACCTGGCCATC	447	Qy
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446		387	Qy
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Search completed: September 14, 1999, 10:07:38 Job time: 915 sec

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US-08-202-056-4
                                                                                                                                     Query Match 100.0%; Score 1737; Best Local Similarity 100.0%; Pred. No. 0; Matches 1737; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 4, Application US/08202056 Patent No. 5440021
                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patin (Generated)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/202,056
FILING DATE: 25-FEB-1994
CLASSIFICATION: 436
FRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/677211
FILING DATE: 29-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: LOVE, RICHARD B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: 706P3
TELEPHONE: 415/225-5530
                                                                                                                                                                                                                                                                                           TELEPHONE: 415/225-55:
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Chuntharapai, Anan APPLICANT: Hebert, Caroline APPLICANT: Kim, Kyung Jin APPLICANT: Lee, James TITLE OF INVENTION: Antibodie NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
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COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
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LENGTH: 1737 bases
TYPE: nucleic acid
STRANDEDNESS: single
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                         GCCACCGCATCTGGAGAACCAGCGGTTACCATGGAGGGGATCAGTATATACACTTCAGAT 120
AACTACACCGAGGAAATGGGCTCAGGGGGACTATGACTCCATGAAGGAACCCTGTTTCCGT
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US-08-153-848-23

PCT-US93-11153-23

US-08-153-848-27

US-08-153-848-31

PCT-US93-11153-27

PCT-US93-11153-27

US-08-202-056-5
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Sequence 23, Appl
Sequence 27, Appl
Sequence 27, Appl
Sequence 31, Appl
Sequence 31, Appl
Sequence 31, Appl
                                                                                                                                        0,
                                                                                                                                        Gaps
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Result

Score

Match

Length

DΒ

Description

Sequence Sequence

US-08-202-056-4
US-08-076-093A-3
US-08-701-265-3
US-08-284-586-3
US-08-805-478-3

sequence sequence sequence sequence sequence sequence sequence

Query

100.0 100.0 100.0 100.0 64.4 111.5 111.5 111.3 110.3 110

PCT-US94-06380-2
PCT-US93-11153-45
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US-08-410-456A-2
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US-08-410-456A-2
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US-08-153-848-1
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US-08-153-848-1
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PCT-US93-03032-4

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3 4 Appli 3 3 Appli 3 3 Appli 4 5 Appli 4 5 Appli 6 6 Appli 1 Appli 1 1 Appli

Pred. No.

55432

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d. No. is the number of results predicted by chance to have a re greater than or equal to the score of the result being printed, is derived by analysis of the total score distribution.

Scoring table:

IDENTITY_NUC

176461 seqs, 45838279 residues

Issued_Patents_NA: *

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GAATTCCAGTGTGCTGGCGG......CCGCCAGCACACTGGAATTC

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nucleic search, using

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GenCore version Copyright (c) 1993 - 1998

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September 14, 1999, 09:52:23; Searc (without 3868.858

Search time 41.16 Seconds

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Million cell updates/sec

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	1201 ACACATTTTTCAGATATAAAAGACTGACCAATATTGTACAGTTTTTATTGCTTGGAT 1260
	1141 TCCAGCTAACACAGATGTAAAAGACTTTTTTTATACGATAAATAA
FILL FILL FRIOR	1081 AAAGGAAAGCGAGGTGGACATTCATCTGTTTCCACTGAGTCTGAGTCTCAAGTTTTCAC 1140
	1021 ACCTCTGCCCAGCACGCACTCACCTCTGTGAGCAGAGGGTCCAGCCTCAAGATCCTCTCC 1080
	961 GCTTTCTCCACTGTTGTCTGAACCCCATCCTCTATGCTTTGCTTGGAGCCAAATTTAAA 1020
	901 AAGCAAGGGTGTGAGTTTGAGAACACTGTGCACAAGTGGATTTCCATCACCGAGGCCCTA 960
	841 TGTTGGCTGCCTTACTACATTGGGATCAGCATCGACTCCTTCATCCTCCTGGAAATCATC 900
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RESULT 2 US-08-076-0 ; Sequence : Datent No	661 CCCAATGACTTGTGGGTGGTTGTGTTCCAGTTTCAGCACATCATGGTTGGCCTTATCCTG 720
<u></u>	601 GACTTCATCTTTGCCAACGTCAGTGAGGCAGATGACAGATATATCTGTGACCGCTTCTAC 660 [
	541 TIGGCIGAAAAGGIGGICIAIGITIGGCGICIGGAICCCIGCCCIG
	481 AGTCTGGACCGCTACCTGGCCATCGTCCACGCCACCAACAGTCAGAGGCCAAGGAAGCTG 540
Db 1501 C	421 GCAGTCCATGTCATCTACACAGTCAACCTCTACAGCAGTGTCCTCATCCTGGGCTTCATC 480
_	361 CTTCCCTTCTGGGCAGTTGATGCCGTGGCAAACTGGTACTTTGGGAACTTCCTATGCAAG 420 [
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	241 ACTGGCATTGTGGGCAATGGATTGGTCATCCTGGTCATGGGTTACCAGAAGAAACTGAGA 300
	181 GAAGAAAATGCTAATTTCAATAAAATCTTCCTGCCCACCATCTACTCCATCATCTTCTTA 240
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e 3, Application US/08076093A
No. 5543503
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US-08-076-093A-3

Sequence 3, Application US/08076093A

Patent No. 5543503

GENERAL INFORMATION:
APPLICANT: Chuntharapai, Anan
APPLICANT: Hebert, Caroline
APPLICANT: Hebert, Caroline
APPLICANT: Hebert, Caroline
APPLICANT: Jin Kim, K.

ITILE OF INVENTION: Antibodies to Human PF4A Receptors
NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURENT APPLICATION DATA:
APPLICATION NUMBER: US/08/076,093A
FILING DATE: 11-Jun-1993
CLASSITICATION NUMBER: 07/810782
FILING DATE: 19-DEC-1991
PRIOR APPLICATION NUMBER: 07/677211
FRIOR DATE: 19-DEC-1991
ATTORNEY/AGGENT INFORMATION:
NAME: Love, Richard B
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: 706P2
TELECOMMUNICATION INFORMATION:

```
: TELEPHONE: 415/225-5530
: TELEFAX: 415/952-9881
: TELEX: 910/371-7168
: INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
: ELNGTH: 1737 nucleotides
TYPE: Nucleic Acid
: TYPE: Nucleic Single
: TOPOLOGY: Linear
US-08-076-093A-3
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                                                     GACTTCATCTTTGCCAACGTCAGTGAGGCAGATGACAGATATATCTGTGACCGCTTCTAC
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                GGCCACCAGAAGCGCAAGGCCCTCAAGACCACAGTCATCCTCATCCTGGCTTTCTTCGCC
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Pred. No. 0;
O; Mismatches
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RESULT 3
US-08-701-265-3
US-08-701-265-3
Sequence 3, Application US/08701265
Patent No. 5776457
GENERAL INFORMATION:
APPLICANT: Lee_LIAMES
APPLICANT: Lee_LIAMES
APPLICANT: Hebert, Caroline
APPLICANT: Jin Kim, K
ITITLE OF INVENTION: Antibodies to
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.

to Human

PF4A

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                GTTTTTCCTGTTCTTAAGACGTGATTTTGCTGTAGAAGATGGCACTTATAACCAAAGCCC
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TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:

NAME: Love, Richard B
REGISTRATION UNMER: 34,659
REFERENCE/DOCKET NUMBER: 706P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-5530
TELEPAX: 415/952-9881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 07/810782
FILING DATE: 19-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/677211
FILING DATE: 29-MAR-1991
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APPLICATION NUMBER: 08/0
FILING DATE: 11-Jun-1993
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MEDIUM TYPE: 3.5 inc
COMPUTER: IBM PC com
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LENGTH: 1737 nucleotides
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TYPE: Nucleic Acid
STRANDEDNESS: Single
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FILING DATE: 22-AUG
CLASSIFICATION: 424
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1 GTTTTTCCTGTTCTTAAGACGTGATTTTGCTGTAGAAGATGGCACTTATAACCAAAGCCC 1560	Qу 150 рь 150	
GCTAGAAATGATCCCCAGCTGTTTATGCATAGATAATCTCTCCCATTCCCGTGGAAC 15	44	
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1 TITGTTTCATATTGATGTGTGTCTAGGCAGGACCTGTGGCCAAGTTCTTAGTTGCTGTAT 138	Db 132	
TTGTTTCATATTGATGTGTGTCTAGGCAGGACCTGTGGCCAAGTTCTTAGTTGCTGTA	132	
1 TTTTGTCTTGTGTTTTCTTTAGTTTTTTGTGAAGTTTAATTGACTTATTTAT	126	
TTTGTCTTGTGTTTTAGTTTTTGTGAAGTTTAATTGACTTATTTAT	12	
1 ACACATTTTTCAGATATAAAAGACTGACCAATATTGTACAGTTTTTATTGCTTGGTTGG	120	
CACATTTTTCAGATATAAAAGACTGACCAATATTGTACAGTTTTTATTGCTTGGTTGG	Qy 120	
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CCAGCTAACACAGATGTAAAAGACTTTTTTTTATACGATAAATAA	Qy 114	
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AAGGAAAGCGAGGTGGACATTCATCTGTTTCCACTGAGTCTGAGTCTTCAAGTTTTTCA	Qy 108	
1 ACCTCTGCCCAGCACGCACTCACCTCTGTGAGCAGAGGGTCCAGCCTCAAGATCCTCTCC 108	Db 102	
CCTCTGCCCAGCACGCACTCACCCTCTGTGAGCAGAGGGTCCAGCCTCAAGATCCTCTC	102	
1 GCTTTCTTCCACTGTTGTCTGAACCCCATCCTCTATGCTTTCCTTGGAGCCAAATTTAAA 102	Db 96	
CTTTCTTCCACTGTTGTCTGAACCCCATCCTCTATGCTTTCCTTGGAGCCAAATTTAA	96	
1 AAGCAAGGGTGTGAGTTTGAGAACACTGTGCACAAGTGGATTTCCATCACCGAGGCCCTA 960	90	
CAAGGGTGTGAGTTTGAGAACACTGTGCACAAGTGGATTTCCATCACCGAGGCCC	90	
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GTTGGCTGCCTTACTACATTGGGATCAGCATCGACTCCTTCATCCTCCTGGAAATCA	84	
1 GGCCACCAGAAGCGCCAGGACCCCCAAGACCACCAGTCATCCTCATCCTCGCCTTTCTTCGCC 840	78	
GCCACCAGAAGCGCAAGGCCCTCAAGACCACAGTCATCCTCATCCTGGCTTTCTTCG	7	
1 CCTGGTATTGTCATCCTGTCCTGCTATTGCATTATCATCTCCAAGCTGTCACACTCCAAG 780	Db 72	
CTGGTATTGTCATCCTGTCCTGCTATTGCATTATCATCTCCAAGCTGTCACACTCCAA	72	
1 CCCAATGACTTGTGGGTGGTTGTGTTCCAGTTTCAGCACATCATGGTTGGCCTTATCCTG 720	Db 66	
CCAATGACTTGTGGGTGGTTGTGTTTCCAGTTTCAGCACATCATGGTTGGCCTTATCCT	66	
1 GACTTCATCTTTGCCAACGTCAGTGAGGCAGATGACAGATATATCTGTGACCGCTTCTAC 660		
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1 TIGGCTGAAAAGGTGGTCTAIGTTGGCGTCTGGATCCCTGCCCTCCTGCTGACTAITTCCC 600		
TGGCTGAAAAGGTGGTCTATGTTGGCGTCTGGATCCCTGCCTG	54	
1 AGTCTGGACCGCTACCTGGCCATCGTCCACGACCAACAGTCAGAGGCCAAGGAAGCTG 540	48	
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PRIOR APPLICATION: 42*
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/076,093
FILING DATE: 11-Jun-1993
APPLICATION NUMBER: 07/810782
FILING DATE: 19-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/677211
FILING DATE: 29-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: LOVE, Richard B
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: 706P2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-5530
TELEEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1737 nucleotides
TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Linear
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Patent No. 5840856
GENERAL INFORMATION:
APPLICANT: Chuntharapai
APPLICANT: Lee, James
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US-08-284-586-3
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                                                   Query Match
Best Local Similarity
Matches 1737; Conserv
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MEDIUM TYPE: 3.5 inch, 1.44 mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/284,586
FILING DATE:
CLASSIFICATION: 424
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TITLE OF INVENTION: Antibodies to
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blv
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
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                                                                                                        NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION DATA:
                       APPLICATION NUMBER: US/08/805.4
FILING DATE: 25-Feb-1997
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/284586
FILING DATE: 10-AUG-1994
                                                                                                                                                                                                                                                                                                        APPLICANT: Lee, James
APPLICANT: Lee, James
APPLICANT: Hebert, Caroline
APPLICANT: Jin Kim, K.
TITLE OF INVENTION: ANTIBODI
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PRIOR APPLICATION DATA: APPLICATION NUMBER:
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NAME: LOVE, RICHARD B.

NAME: LOVE, RICHARD B.

REGISTRATION NUMBER: 94,659

REFERENCE/DOCKET NUMBER: P0706

TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-5530

TELEFAX: 415/952-9881

TELEX: 910/371-7168

INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1737 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Linear
US-08-805-478-3
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Best Local Similarity
Matches 1737; Conserv
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APPLICATION NUMBER: 07/8:
FILING DATE: 19-DEC-1991
ATTORNEY/AGENT INFORMATION:
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RESULT 6
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; GENERAL INFORMATION:

Application

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REFERENCE/DOCKET NUMBER: 706F
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-5530
TELEPAX: 415/952-9881
TELEYAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1737 bases
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Best Local Similarity
Matches 1737; Conserv
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APPLICANT: Lee, Jame
APPLICANT: Hebert, on
APPLICANT: K. Jin K.
APPLICANT: Genentecl
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 kb floppy
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 11-JUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-SOFTWARE: patin (Genentech) CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
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STREET: 460 Point San Bruu
CITY: South San Francisco
STATE: California
COUNTRY: USA
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE:
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                                                             AGCATGACGGACAAGTACAGGCTGCACCTGTCAGTGGCCGACCTCCTCTTTGTCATCACG
                                                                                                                                                                       GAAGAAAATGCTAATTTCAATAAAATCTTCCTGCCCACCATCTACTCCATCATCTTTA
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              CTTCCCTTCTGGGCAGTTGATGCCGTGGCAAACTGGTACTTTGGGAACTTCCTATGCAAG
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460 Point San Bruno
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Hebert, Car
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Query Match
Best Local Similarity
Matches 1131; Conserv

Conservative

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64.48; 99.68;

Score 1118.2; Pred. No. 1.5 Mismatches

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US-08-153-848-45
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US-08-153-848-45
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                                                                              REFERENCE/DOCKET NUMBER: 3179
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEY. 25-3856
INFORMATION FOR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:
LENGTH: 1317 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 45,
Patent No. 5
                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/977.
APPLICATION UNMBER: US 07/977.
FILING DATE: 17-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: NO. 5759804and, Greta E
REGISTRATION NUMBER: 35,302
REGISTRATION NUMBER: 35,302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 60606

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Godiska, Ronald
APPLICANT: Gray, Patrick W.
APPLICANT: Schweikart, Vicki L.
TITLE OF INVENTION: No. 5759804el Seven Transmembrane
NUMBER OF SEQUENCES: 64
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                                                   MOLECULE TYPE: FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Chicago
STATE: Illinoi
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GTTTTTCCTGTTCTTAAGACGTGATTTTGCTGTAGAAGATGGCACTTATAACCAAAGCCC 1560
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                                                                    CTCAAGATCCTCTCCAAAGGAAAGCGAAGGTGGACATTCATCTGTTTTCCACTGAGTCTGAG
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PCT-US93-11153-45
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PCT-US93-11153-45
Sequence 45, Application
GENERAL INFORMATION:
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Best Local Similarity
                                                                                                                                                                                                                                Matches
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 45:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: DC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0:
FILING DATE: 17-NOV-1992
ATTORNEY/AGENT INFORMATION:
AUTHOR WALLS!
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LENGTH: 1317 base pairs
TYPE: nucleic acid
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APPLICATION NUMBER: PC
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APPLICANT: Schweikart, Vicki L.
TITLE OF INVENTION: Novel Seven
                                                                                                                                                                                                                                                                                                                                                FEATURE:
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Chicago
STATE: Illinois
COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                     ATATACACTTCAGATAACTACACCGAGGAAATGGGCTCAGGGGACTATGACTCCATGAAG 165
             CAGAAGAAACTGAGAAGCATGACGGACAAGTACAGGCTGCACCTGTCAGTGGCCGACCTC
                                                                                                             CAGAAGAAACTGAGAAGCATGACGGACAAGTACAGGCTGCACCTGTCAGTGGCCGACCTC
                                                   GAACCCTGTTTCCGTGAAGAAAATGCTAATTTCAATAAAATCTTCCTGCCCACCATCTAC 225
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                                                                                                                                                                                                                          Score 1118.2; DB 5;
Pred. No. 1.5e-224;
Pred. No. 1.5e-324;
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RESULT 9
PCT-US95-03032-1
                                                                                                                                                       Sequence 1, Application GENERAL INFORMATION:
                                    APPLICANT: Repligen Corporation
APPLICANT: the Trustees of Boston University
TITLE OF INVENTION: ANTIBODIES TO INTERLEUKIT
TITLE OF INVENTION: METHODS OF USE
NUMBER OF SEQUENCES: 9
                        CORRESPONDENCE ADDRESS:
ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CTCAAGATCCTCTCCAAAGGAAAGCGAGGTGGACATTCATCTGTTTCCACTGAGTCTGAG
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Fish & Richardson
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                                                                                        INTERLEUKIN-8
                                                                                           RECEPTORS
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Best Local S
Matches 456
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SEQUENCE CHARACTERISTICS:
LENGTH: 1200
TYPE: nucleic acid
STRANDEDNESS: Single
TOPOLOGY: line*
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MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 502 or 555X
OPERATING SYSTEM: IBM P.C. DOS (Version 3.50)
SOFTWARE: WordPerfect (Version 5.0)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/03032
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 08/237,937

FILING DATE: 02-MAY-94

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/210,250

FILING DATE: 15-MAR-94

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/803,842

FILING DATE: 09-DEC-91

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/726,606

FILING DATE: 09-JUL-91

PRIOR APPLICATION DATA:
APPLICATION DATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REGISTRATION NUMBER: 32,983
REFERENCE/DOCKET NUMBER: 04
TELECOMMUNICATION INFORMATION:
TELECHONE: (617) 542-5070
TELECAX: (617) 542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 225 FI
CITY: Boston
STATE: Massach
COUNTRY: U.S.A
ZIP: 02110-280
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les 456; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TCAATAAATCTTCCTGCCCACCATCTACTCCATCATCTTTAACTGGCATTGTGGGCA 256
                                                                                                                                                                                                                                                                               ACAGGCTGCACCTGTCAGTGGCCGACCTCCTTTGTCATCACGCTTCCCTTCTGGGCAG
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    TGGCCATTGTCCATGCTACTCGCACACTGACCCAGAAGCGCCACTTG--
                                                  TGGCCATCGTCCACGCCACCAACAGTCAGAGGCCCAAGGAAGCTGTTGGCTGAAAAGGTGG
                                                                                                                                                                                                                                 TTGATGCCGTGGCAAACTGGTACTTTGGGAACTTCCTATGCAAGGCAGTCCATGTCATCT 436
                                                                                                                                                                                                                                                                                                                                                                            ACTCCCTGGTGATGCTGGTCATACTGTACAGCCGGAGCAACCGTTCGGTCACCGACGTCT
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                                                                                             ACACAGTCAACCTCTACAGCAGTGTCCTCATCCTGGCCTTCATCAGTCTGGACCGCTACC
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PCT-US92-02977-6
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TELEFAX: (61/) ...
TELEX: 200154
INFORMATION FOR SEQ ID NO: 6
SEQUENCE CHARACTERISTICS:
FRIGHH: 1373
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                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 50Z or 55SX
OPERATING SYSTEM: IBM P.C. DOS (Version
SOFTWARE: WordPerfect (Version 5.0)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                   REFERENCE/DOCKET NUMBER: 00
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEPEAX: (617) 542-8906
                                                                                                                                                          APPLICATION NUMBER: 07/685,101 FILING DATE: April 10, 1991 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1009
                                                                                                                                                                                                      PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
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                                                                                                           NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
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CLASSIFICATION:
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STATE: Massa
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Fish & Richardson
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METHODS
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INTERLEUKIN-8 RECEPTORS
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; STRANDEDNESS: Single
; TOPOLOGY: linear
PCT-US92-02977-6
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Best Local
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                                                           GCCACCGAGATTCTGGGCTTCCTGCACAGCTGCCTCAACCCCATCATCTACGCCTTCATT
                                                                          ATCACCGAGGCCCTAGCTTTCTTCCACTGTTGTCTGAACCCCATCCTCTATGCTTTTCCTT 1005
                                                                                                                       AGGACCCACGTGATCCAGGAGACGTGTGAGCGCCCCAATGACATTGACCGGGCCCTGGAC
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Similarity 54.8%;
                             1017
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 201.2; DB 5; Pred. No. 1.1e-33;
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RESULT 11 PCT-US95-03032-3

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Best Local Similarity
Matches 467; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REGISTRATION NUMBER: 32,983
REFERENCE/DOCKET NUMBER: 04,
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEFAX: (617) 542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 502 or 555X
OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)
SOFTWARE: WordPerfect (Version 5.0)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Repligen Corporation
APPLICANT: the Trustees of Boston University
TITLE OF INVENTION: ANTIBODIES TO INVERLEUKIN-8 RECEPTORS
TITLE OF INVENTION: METHODS OF USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 09-JUL-91
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: 08
FILING DATE: 02-MAY-94
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 10-APR-91
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
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APPLICATION NUMBER:
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STRANDEDNESS: single
TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: 07/803,842 FILING DATE: 09-DEC-91
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: PCT/US95/03032 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE: Massachusetts COUNTRY: U.S.A.
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ATCACGCTTCCCGTCTGGGCAGTTGATGCCGTGGCAAACTGGTACTTTGGGAACTTCCTA 414
                                                                                                                                                    TTCTTAACTGGCATTGTGGGCAATGGATTGGTCATCCTGGTCATGGGTTACCAGAAGAAA
                                                                                                                                                                                                      TGCCGGTCAGAATCTCTGGAAACCAACAGCTATGTTGTGCTCATCACCTATATCCTGGTC 238
                                                                                                                                                                                                                              TTCCGTGAAGAAATGCTAATTTCAATAAAATCTTCCTGCCCACCATCTACTCCATCATC
                                                       ACCTGCTCGGTCACCGACGTCTACCTGCTGAACCTGGCCATCGCCGACCTGCTCTTTGCC
                                                                                          CTGAGAAGCATGACGGACAAGTACAGGCTGCACCTGTCAGTGGCCGACCTCCTTTGTC
                                                                                                                               TTCCTGCTGAGCCTGCGGCAACTCCCTGGTGATGCTGGTCATCCTGTACAGCCGGAGC
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225 Franklin Street
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Conservative
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54.8%;
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Pred. No. 1.1e-33;
0; Mismatches 373;
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                                 ZIP: UZIIV ZUE FORM:
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 50Z or 55SX
OPERATING SYSTEM: IBM P.C. DOS (Version 3.
SOFTWARE: WordPerfect (Version 5.0)
CURRENT APPLICATION DATA:
CORRENT APPLICATION DATA:
CORREST APPLICATION NUMBER: PCT/US92/02977
                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1, Applicati
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1016
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TITLE OF INVENTION:
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PRIOR APPLICATION DATA:
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                FILING DATE: 1 CLASSIFICATION:
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N: 435
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TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
PCT-US92-02977-1
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Best Local Similarity 54.5
Matches 452; Conservative
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FILING DATE: APril 10, 1991
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/POCKET NUMBER: 00231/0
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (617) 542-89
TELEX: 200154
INFORMATION FOR SEQ ID NO:
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908 GGTGTGAGTTTGAGAACACTGTGCACAAGTGGATTTCCACCGAGGGCCCTAGCTTTCT
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                                                                                                                                              AGAAGCGCAAGGCCCTCAAGACCACAGTCATCCTCATCCTGGCTTTCTTCTTCGCCTGTTGGC
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                                                   TGCCCTACAACCTGGTCCTGCTCGCAGACACCCTCATGAGGACCCACGTGATCCAGGAGA
                                                                                     TGGTCATGCTGTTTTGCTATGGGTTCACCCGTCGCACGCTGTTCCAGGCCCACATGGGGC
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                                                                                                                        AGGAAGTCAACTTCTACAGTGAAATCCTGCTCCTGGCCTGCATCAGTGTGGACCGCTACC
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Pred. No. 1.5e-33;
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                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 455; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/202,056
FILING DATE: 25-FEB-1994
CLASSIFICATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/677211
FILING DATE: 29-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: LOVE, Richard B.
REGISTRATION NUMBER: 34,659
REGISTRATION NUMBER: 34,659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 1883 bases
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Kim, Kyung Jin
APPLICANT: Lee, James
TITLE OF INVENTION: Antibodies
NUMBER OF SEQUENCES: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION: TELEPHONE: 415/225-5530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Chuntharapai, Ana APPLICANT: Hebert, Caroline
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
                        363 TCCCTTCTGGGCAGTTGATGCCGTGGCAAACTGGTACTTTGGGAACTTCCTATGCAAGGC 422
                                                                                                   303 CATGACGGACAAGTACAGGCTGCACCTGTCAGTGGCCGACCTCCTCTTTTTCACGCT
                                                                            216 CGTCACTGATGTCTACCTGCTGAACCTGGCCTTGGCCGACCTACTCTTTGCCCTGACCTT
                                                                                                                                                                                  243 TGGCATTGTGGGCAATGGATTGGTCATCCTGGTCATGGGTTACCAGAAGAAACTGAGAAG 302
                                                                                                                                                                                                                                                                            183 AGAAAATGCTAATTTCAATAAAATCTTCCTGCCCACCATCTACTCCATCATCTTCTTAAC 242
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CITY: South San Francisco
STATE: California
COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 1883 bases
TYPE: nucleic acid
STRANDEDNESS: single
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GCCCATCTGGGCCGCCTCCAAGGTGAATGGCTGGATTTTTGGCACATTCCTGTGCAAGGT
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                                                                                                                                                                                                                                                                                                                   Score 196.8; DB 1;
Pred. No. 9.8e-33;
0; Mismatches 377;
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US-08-076-093A-1
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APPLICANT: Chuncharapai
APPLICANT: Lee, James
APPLICANT: Hebert, Carc
APPLICANT: Jin Kim, K.
                                                                                                                                                                                                                                                                                                                                                                    Sequence 1, Application US/08076093A Patent No. 5543503
                                       COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb 1
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS,MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
                                                                                                                                                                                                                                                       APPLICANT: Jin Kim, K.
TITLE OF INVENTION: Antibodies
NUMBER OF SEQUENCES: 6
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APPLICATION NUMBER: US/08/076,093A FILING DATE: 11-Jun-1993 CLASSIFICATION: 530
                                                                                                                                              ZIP:
                                                                                                                                                           COUNTRY:
                                                                                                                                                                         STREET: 460 Point San Bruno
CITY: South San Francisco
STATE: California
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                                                                                                          1.44 Mb floppy disk
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US-08-076-093A-1
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TELEFAX: 415/952-9881
TELEFAX: 415/952-9881
TELEFAX: 910/371-7188
INFORMATION FOR SED ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1933 nucleotides
TYPE: Nucleic Acid
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Best Local Similarity
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REFERENCE/DOCKET NUMBER: 70
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: 07/677211
FILING DATE: 29-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/8
FILING DATE: 19-DEC-1991
PRIOR APPLICATION DATA:
834 CTTCGCCTGTTGGCTGCCTTACTACATTGGGATCAGCATCGACTCCTTCATCCTCCTGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      183 AGAAAATGCTAATTTCAATAAAATCTTCCTGCCCACCATCTACTCCATCATCTTCTTAAC 242
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Pred. No. 9.8e-33;
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                                                                                                                   Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: 70
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-5530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: 08/2: FILING DATE: 28-APR-1994 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION: NAME: Love, Richard B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Lee, James,
APPLICANT: Holmes, William E.,
APPLICANT: Woods, William I.
TITLE OF INVENTION: Human PF4A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Love, Richard B
REGISTRATION NUMBER:
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CITY: South San Francisco
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                                                    AGAAAATGCTAATTTCAATAAAATCTTCCTGCCCACCATCTACTCCATCATCTTTAAC 242
TGGCATTGTGGGCAATGGATTGGTCATCCTGGTCATGGGTTACCAGAAGAAACTGAGAAG 302
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24-MAR-1995
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Pred. No. 9.8e-33;
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Search completed: Job time: 106 sec

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                                                             GATTCTGGGATTTCTCCATAGCTGCCTCAACCCCATCATCTACGCCTTCATCGGCCAAAA 982
                                                                                                                              GGTGATCCAGGAGACCTGTGAGCGCCGCCAACAACATCGGCCGGGCCCCTGGATGCCCACTGA 922
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em_est26:*	em_est25:*		•••	

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

ALIGNMENTS

ACCESSION NID	DEFINITION	Locus	AA707668/c	RESULT 1
PROTEIN-COUPLED RECEPTOR LCR1 HOMOLOG (HUMAN);, mRNA sequence. AA707668 g2717586	<pre>zj29f12.s1 Soares_fetal_liver_spleen_lNFLS_S1 Homo sapiens cDNA clone IMAGE:451727 3' similar to gb:L06797 PROBABLE G</pre>	AA707668 786 bp mRNA EST 24-DEC-1997		

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BASE COUNT
ORIGIN
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                                                                                                                                                                                                                             942
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nes 728; Conserv
CTGAGTCTTCAAGTTTTCACTCCAGCTAACACAGATGTAAAAGACTTTTTTTATACGAT 1180
                                                                                    CCAGCCTCAAGATCCTCCCAAAGGAAAGCGAGGTGGACATTCATCTGTTTCCACTGAGT 1120
                                                                                                                                                                                                                                                             CATCCTCCTGAAAAAATCCACCCAGAGGTGGCA--TTGAACACCCCGTGCACCACAGGAT 729
                                                    TCCTTGGAGCCAAATTTAAAACCTCTGCCCAGCACGCACTCACCTCTGTGAGCAGAGGGT 1060
                                                                                                                                                                                         TCCAATCATCGAGGCCCGAGCTTTCCTCCACTAGTTGTCAGACCACCATCCTATATGCTA 669
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                                                                                                                        TCTTGGGGCCAATATTTACAACCTCTGCCAAGCACGCACTCACCTCTGTGAGCAGAGGGT
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1 (bases 1 to 786)
Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B., White,T., Wylie,T., Waterston,R. and Wilson,R. WashU-NCI human EST Project
Unpublished (1997)
On Nov 6, 1997 this sequence version replaced g1:315382.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@mage.llnl.gov) for further information.
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 268.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4444 Forest Park Parkway, Box 8501, St. Louis, Tel: 314 286 1800 Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Wilson RK
Washington University School of Medicine
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Eukaryota; M
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/map="17; 15q26.1"
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/db_xref="GDB:1388083"
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                                                                                                                                                                                                                                                                                                                                                                                              AA781110 792 bp mRNA 31-aj23e10.s1 Soares_testis_NHT Homo sapiens cDNA clone similar to gb:L06797 PROBABLE G PROTEIN-COUPLED RECEPHOMOLOG (HUMAN);, mRNA sequence.
                                                                                                                                                                    Tumor Gene Index
Unpublished (1997)
On Sep 12, 1996 th
                                                                                    cDNA Library Preparation:
                                                                                                       Email:
                                                                                                                   Contact: Robert Strausberg, Tel: (301) 496-1550
                                                                                                                                                                                                                 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap
National Cancer Institute, Cancer Genome Anat
                                                                                                                                                                                                                                                     Eutheria; Primates; 1 (bases 1 to 792)
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CDNA Library Arrayed by: Greg Lennon; Ph.D.
DNA Sequencing by: Washington University Genome
Clone distribution: NCI-CGAP clone distribution
cound through the I.M.A.G.E. Consortium/LLNL at:
                                                                                  Robert_Strausberg@nih.gov
lbrary Preparation: M. Bento
                                                                                                                                                                                                                                                                                                                                                         GI:2840441
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                                                    ATCTCTCCATTCCCGTGGAACGTTTTTCCTGTTCTTAAGACGTGATTTTTGCTGTAGAAGA 1539
                                                                                                    CAGAGCGTGTAGTGAATCACGTAAAGCTAGAATGATCCCCAGCTGTTTATGCATAGATA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
was prepared from mRNA obtained from Clontech
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95.2%;
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Pred. No. 5.2e-108;
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AA634211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL;
IMAGE Consortium (info@image.llnl.gov) for further i
Insert Length: 835 Std Error: 0.00
Seq primer: -40n13 fwd. ET from Amersham
High quality sequence stop: 393.
Location/Qualifiers
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4444 Forest Park Parkway,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WashU-NCI human EST Project Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Krizman,D., Kucaba,T., Lacy,M., Le.N., Lennon,G., Marra,M., Karizman,D., Kucaba,T., Lacy,M., Le.N., Lennon,G., Marra,M., Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R.
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/lab_host="SOLR cells (kanamycin resistant)"
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/db_xref="taxon:9606"
/clone="IMAGE:868115"
                                                                                                                                                                                                                                                                                                                                                                                             /sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                             /clone_lib="Stratagene lung (#937210)"
                                                                                                                                    34.9%;
94.0%;
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Pred. No. 9.9e-101;
0; Mismatches 40;
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way, Box 8501, St. Louis,
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                                                Tel: (301) 496-1550
Email: Robert Strausberg,
                                                                                                                                                                                                                                     A1493618 657 bp mRNA EST 30-MAR-1999 h139e07:x1 NCI_CGAP_PAnl Homo sapiens cDNA clone IMAGE:2120676 similar to gb:L06797 PROBABLE G PROTEIN-COUPLED RECEPTOR LCR1 HOMOLOG (HUMAN);, mRNA sequence.
Life Technologies catalog #: 11548-013
DNA Sequencing by: Washington University Genome
Clone distribution: NCI-CGAP clone distribution
found through the I.M. A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
                                                                                              Unpublished (1997)
On May 18, 1998 th
                                                                                                                  NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy
Tumor Gene Index
                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 657)
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AI493618.1
                                                                                                                                                                                    Homo sapiens
                                                    Robert_Strausberg@nih.gov
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High quality sequence stop: '
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Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.72 kb. Life Technologies catalog #:
11548-013"
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/clone_lib="NCI_CGAP_Pan1"
/tissue_type="adenocarcinoma"
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/db_xref="taxon:9606"
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                                                                                                            CAA--GGAAAGCGAGTGGACATTCATCTGTTTCCACTGAGTCTGAGTCTTCAAGTTTTCA 533
                                                                                                                                                                                                                         AAAAACCTCGCCCAGACGCACTACACCTTGTGAGCAGA-GGTCCAGCCTCAAGATCCTCTC 591
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Hiller,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R. Washu-NCI human EST Project
Unpublished (197)
On Sep 12, 1996 + hin-
                               TACACATTTTTCAGATATAAAAGACTGACCAATATTGTACAGTTTTTATTGCTTGGTAGGA
                                                                                           AA634201 651 bp mRNA
ac72a07.sl Stratagene lung (#937210)
IMAGE:868116 3' similar to gb:L06797
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Seq primer: -40ml3 fwd. ET from Amersham High quality sequence stop: 413.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4444 Forest Park Parkway,
Tel: 314 286 1800
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Wilson RK Washington University
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/db_xref="taxon:9606"
/clone="IMAGE:886116"
/clone_lib="Stratagene lung (#937210)"
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96.3%;
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Pred. No. 3.7e-98;
0; Mismatches 21;
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Homo sapiens cDNA clone
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Entheria; Primates; Catarrhini; Hominidae; Homo.
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On Jan 17, 1998 th
                                                                                                                                                                                                                                                                                                                                                            High quality sequence stop:
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National Cancer Institute, Cancer Genome Anatomy
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/note="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (fetal lung NbHL19W, testis NHT, and B cell NCI_CGAP_GCB1) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 297480-302087, 682632-687239,
                                                                                                                                                                                                            /clone_lib="Soares_NFL_T_GBC_S1"
/lab_host="DH10B"
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similar to gb:L06797 PROBABLE G PROTEIN-COUPLED RECEPTOR LCR1
HOMOLOG (HUMAN);, mRNA sequence.
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Soares and M. Fatima Bonaldo. "
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Pred. No. 1.5e-97;
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -28m13 rev2 ET from Amersham
                                CCTGTTCTTAAGACGTGATTTTGCTGTAGAAGATGGCACTTATAACCAAAGCCCAAAGTG
                                                   CCTGTTCTTAAGACGTGATTTTGCTGTAGAAGATGGCACTTATAACCAAAGCCCAAAGTG
                                                                                                TAGAAATGATCCCCAGCTGTTTATGCATAGATAATCTCTCCATTCCCGTGGAACGTTTTT
                                                                                                                 TAGAAATGATCCCCAGCTGTTTATGCATAGATAATCTCTCCCATTCCCGTGGAACGTTTTT 1506
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/tissue_type="pooled human me
pregnant uterus"
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/db_xref="GDB:5977529"
/db_xref="taxon:9606"
/clone="IMAGE:754619"
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Email: Robert Cr
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Unpublished (1997)
On Sep 12, 1996 th
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Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Insert Length: 1159
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CDNA Library Preparation: Stratagene, Inc. CDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Clone distribution: NCI-CGAP Clone distribution found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 593)
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                                                                                                                                                                                                    /tlssue__wpe="breast tumor"
/tlssue_ype="breast tumor"
/tlssue_ype="breast; vector: Bluescript SK-; Site_1:
/note="Organ: breast; vector: Bluescript SK-; Site_1:
ECORI; Site_2: XhoI; Cloned unidirectionally, Primer:
Oligo dT. Ductal breast tumor. 5' adaptor sequence: 5'
GANTTCGGCACGAG, 3' 3' adaptor sequence: 5'
GANTTCGGCACGAG, 3' 3' adaptor sequence: 5'
CTCGAGTTTTTTTTTTTTTTTTTTT 3' Average insert size: 0.9 kb.
a 117 c 95 g 161 t
                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1072327"
/clone_lib="MCI_CGAP_Br3"
                                                                                                                                                                                                                                                                                                                      /sex="female"
                                                                                                                                                                                                                                                                                                                                                                                                            location/Qualifiers
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                                     Insert Length: 742 Sto
Seq primer: -40ml3 fwd.
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            quality sequence stop:
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1648 ATAAAAGTACATGTTAAACTTA 1669
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Unpublished (1997)
On Jan 9, 1998 this sequence version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 556)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Pro
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                                                                          CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome
Clone distribution: NCI-CGAP clone distribution
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                                   Bmail: Robert_Strausberg@nih.gov
Tissue Procurement: Louis M. Staudt,
Ph.D., Gerald Marti, M.D.
CDNA Library Preparation: M. Bento &
                                                                                                                                                                                                                                                                                                                                            Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550
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Std Error: 0.00
wd. ET from Amersham
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                                                                                                              AAAAAAAAAAAAAA 1687
                                                                                                                                                   AGCACCTACAGTGTACAGTCTTGTATTAAGTTGTTAATAAAAGTACATGTTAAACTTAAA 1671
                                                                                                                                                                                                        CCGTGGAACGTTTTTCCTGTTCTTAAGACGTGATTTTGCTGTAGAAGATGGCACTTATAA
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similar to
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/db_xref="taxon:9606"
/clone="IMAGE:1272736"
/clone_lib="NCI_CGAP_GCB1"
/tissue_type="germinal center B continue"/lab_host="DH10B"
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539 bp mRNA EST NCI_CGAP_Lul Homo sapiens cDNA clone gb:L06797 PROBABLE G PROTEIN-COUPLED
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              TTGCTGTATGTCTCGTGGTAGGACTGTAGAAAAGGGAACTGAACATTCCAGAGCGTGTAG 1431
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                                                                                         TAAATTTTTTTTGTTTCATATTGATGTGTGTCTAGGCAGGACCTGTGGCCAAGTTCTTAG 1371
                                                                                                                                      TIGTIGGATTITIGICIIGIGITICTITAGITITIGIGAAGITIAAITGACITATITATA 1311
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                                                                                                                                                                                                                                                                                                             539;
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High quality sequence stop: 432.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: Robert_Strausberg@nih.gov
Tissue Procurement: L. Jeffrey Medeiros, M.D.,
Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tumor Gene Index
Unpublished (1997)
On Sep 12, 1996 th
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy
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Eutheria; Primates;
1 (bases 1 to 539)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Robert Strausberg, Ph.D.
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                                                                                                                                                                                                                                                                                                           Conservative
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/clone="IMAGE:1142297"
/clone_lib="NCI_CGAP_Lul_
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100.0%;
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                                                                                                                                                                                                                                                                                                         Score 539; DB 36;
; Pred. No. 1.7e-88;
0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -28mil rev2 ET from Amersham
High quality sequence stop: 421.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. I
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 521)

Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R. WashU-Merck EST project 1997

Unpublished (1997)

On Sep 12, 1996 this sequence version replaced gi:1393144.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AA479467 521 bp mRNA EST 08-AUG-1997 zv471710.r1 Soares_NhHWPU_S1 Homo sapiens cDNA clone IMAGE:753 similar to gb:LO5797 PROBABLE G PROTEIN-COUPLED RECEPTOR LCR1 HOMOLOG (HUMAN); mRNA sequence.
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           132
/note="Organ: mixed (see below); Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I: Site_2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (melanocyte 2MbHM, pregnant uterus NbHPU, and fetal heart NbHH19W) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 260232-265223, 340488-345479, and 484488-489479."
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                                                                                                                                                                                                                                                                                                  pregnant uterus"
                                                                                                                                                                                                                                                                                                                       /clone_lib="Soares_NhHMPu_S1"
/tissue_type="Pooled human me
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/map="956G09; 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
/db_xref="GDB:5976803"
                                                                                                                                                                                                                                                                          /lab_host="DH10B"
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                                       Email: Robert_Strausberg@nih.gov
Tissue Procurement: Louis M. Staudt,
Ph.D., Gerald Marti, M.D.
                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 55) NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap. National Cancer Institute, Cancer Genome Anatomy Pro
                                                                                                                                                                                                                                                                                                                                           nx85d08.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1269039 Similar to gb:L06797 PROBABLE G PROTEIN-COUPLED RECEPTOR LCR1 HOMOLOG (HUMAN);, mRNA sequence.

AA747545
                                                                                                                                       Unpublished (1997)
On May 18, 1995 this
                Bonaldo,
                                                                                         Contact: Robert Strausberg, Tel: (301) 496-1550
                                                                                                                                                                                                                                                                  Homo sapiens
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                                                                                                                                 CTCCA-TTCCCGTGGAACGTTTTTCCTGTTCTTAAGACGTGATTTTTGCTGTAGAAGATGG 1542
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 www-bio.llnl.gov/bbrp/image/image.html
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/lab_host="DH10B"
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/clone_lib="NCI_CGAP_GCB1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4444 Forest Park Parkway, Box 8501, St. Louis, Tel: 314 286 1800 Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     zo45e12.s1 Stratagene endothelial cell 937223 Homo sapiens cDNA
clone IMAGE:589870 3' similar to gb:L06797 PROBABLE G
PROTEIN-COUPLED RECEPTOR LCR1 HOMOLOG (HUMAN); , mRNA sequence.
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Wilson RK
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/clone="TMACT:"??
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/db_xref="GDB:4621256"
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Pred. No. 1.6e-82;
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                                                                                                                                                                                                                             rel: (301)
Email: Robe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AA804282 536 bp mRNA EST 18-FEB-1998 mw30h06.51 NCI_CGAP_GCBO Homo sapiens cDNA clone IMAGE:1242011 similar to gb:L06797 PROBABLE G PROTEIN-COUPLED RECEPTOR LCR1 HOMOLOG (HUMAN);, mRNA sequence.

AA804282
                                                                                                              Email: Robert_Strausberg@nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.,
Ph.D., Gerald Marrii, M.D.
CDNA Library Preparation: Louis M. Staudt, M.D.,
cDNA Library Preparation: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome S
Clone distribution: NCI-CGAP clone distribution if
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550
                                                                                                                                                                                                                                                                                                Unpublished
On Jan 14, 1
                                                                                                                                                                                                                                                                                                                               Tumor Gene Index
                                                                                                                                                                                                                                                                                                                                               NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy
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Eutheria; Primates;
1 (bases 1 to 536)
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                                              Insert Length: 1513
Seq primer: -40m13 i
                                                                                                www-bio.llnl.gov/bbrp/image/image.html
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             primer: -40ml3 fwd. ET from Amersham
quality sequence stop: 486.
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14, 1998 this sequence version
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Eukaryota; Me
Eutheria; Pri
                                                                                                                AA426644
g2107314
                                                                                                                                           AA426644 501 bp mRNA EST 16-OCT-1997 zv47h11.s1 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:756837 3' similar to gb:L06797 PROBABLE G PROTEIN-COUPLED RECEPTOR LCR1 HOMOLOG (HUMAN);, mRNA sequence.
                                                                   human.
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theria; Primates; (bases 1 to 501)
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/db_xref="taxon:9606"
/map="21"
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/tissue_type="germinal center B-cells"
/lab_host="SOLR (kanamycin resistant)"
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                                Metazoa;
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98.1%;
                 Chordata; Craniata; Vertebrata; Mammalia; Catarrhini; Hominidae; Homo.
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Matches 501; Conserv
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AGTGAATCACGTAAAGCTAGAAATGATCCCCCAGCTGTTTATGCATAGATAATCTCTCCAT
                                                                                                                                                                                          HITTGCTGTATGTCTCGTGGTAGGACTGTAGAAAAGGGAACTGAACATTCCAGAGCGTGT
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Unpublished (1997)
On Apr 14, 1993 this sequence version replaced gi:693425.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: estewatson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -41m13 fwd. ET from Amersham
High quality sequence stop: 332.
Location/Qualifiers
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Washington University School of Medicine
444 Forest Parkway, Box 8501, St. Louis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tel: 314 286 1800
Fax: 314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone="IMAGE:756837"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            tissue_type="ovarian tumor"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone_lib="Soares ovary tumor NbHOT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                 28.8%; Score 501; DB 33; Length 501; 100.0%; Pred. No. 1.3e-81; tive 0; Mismatches 0; Indels
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